

Seq. No. 5799
 Contig ID 5445_2.R1040
 5'-most EST LIB3050-012-Q1-E1-G5

Seq. No. 5800
 Contig ID 5445_3.R1040
 5'-most EST pxt700942928.h1

Seq. No. 5801
 Contig ID 5445_4.R1040
 5'-most EST uxk700668613.h1

Seq. No. 5802
 Contig ID 5447_1.R1040
 5'-most EST LIB3028-001-Q1-B1-D8

Seq. No. 5803
 Contig ID 5448_1.R1040
 5'-most EST fC-gmse7000756618r1
 Method BLASTX
 NCBI GI g4006924
 BLAST score 267
 E value 4.0e-23
 Match length 60
 % identity 75
 NCBI Description (Z99708) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No. 5804
 Contig ID 5448_2.R1040
 5'-most EST fC-gmse700756174a2
 Method BLASTX
 NCBI GI g2580440
 BLAST score 293
 E value 4.0e-26
 Match length 81
 % identity 72
 NCBI Description (D87261) PCF2 [Oryza sativa]

Seq. No. 5805
 Contig ID 5448_3.R1040
 5'-most EST uC-gmropic030d07b1
 Method BLASTN
 NCBI GI g2580437
 BLAST score 68
 E value 9.0e-30
 Match length 164
 % identity 85
 NCBI Description Oryza sativa mRNA for PCF1, complete cds

Seq. No. 5806
 Contig ID 5448_4.R1040
 5'-most EST g5753241

Seq. No. 5807
 Contig ID 5448_5.R1040

5'-most EST fC-gmse7000756174f1
 Method BLASTX
 NCBI GI g2979559
 BLAST score 145
 E value 9.0e-21
 Match length 171
 % identity 40
 NCBI Description (AC003680) putative DNA binding protein [Arabidopsis thaliana]

Seq. No. 5808
 Contig ID 5448_6.R1040
 5'-most EST LIB3170-017-Q1-K1-H11
 Method BLASTX
 NCBI GI g2580440
 BLAST score 300
 E value 4.0e-27
 Match length 74
 % identity 74
 NCBI Description (D87261) PCF2 [Oryza sativa]

Seq. No. 5809
 Contig ID 5449_1.R1040
 5'-most EST LIB3028-001-Q1-B1-E11
 Method BLASTX
 NCBI GI g2245108
 BLAST score 382
 E value 1.0e-36
 Match length 157
 % identity 52
 NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No. 5810
 Contig ID 5451_1.R1040
 5'-most EST ssr700559029.h1

Seq. No. 5811
 Contig ID 5451_2.R1040
 5'-most EST LIB3028-001-Q1-B1-B6

Seq. No. 5812
 Contig ID 5452_1.R1040
 5'-most EST LIB3030-005-Q1-B1-C12
 Method BLASTX
 NCBI GI g2661840
 BLAST score 1216
 E value 1.0e-134
 Match length 340
 % identity 66
 NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]

Seq. No. 5813
 Contig ID 5452_2.R1040
 5'-most EST xpa700797523.h1
 Method BLASTX
 NCBI GI g2244759
 BLAST score 2192

E value 0.0e+00
 Match length 489
 % identity 79
 NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No. 5814
 Contig ID 5452_6.R1040
 5'-most EST asn701131792.h1
 Method BLASTX
 NCBI GI g2244760
 BLAST score 616
 E value 4.0e-64
 Match length 151
 % identity 73
 NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No. 5815
 Contig ID 5452_7.R1040
 5'-most EST hyd700729029.h1
 Method BLASTX
 NCBI GI g2661840
 BLAST score 329
 E value 1.0e-30
 Match length 98
 % identity 59
 NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]

Seq. No. 5816
 Contig ID 5454_1.R1040
 5'-most EST dpv701099580.h1

Seq. No. 5817
 Contig ID 5454_2.R1040
 5'-most EST LIB3028-001-Q1-B1-C1

Seq. No. 5818
 Contig ID 5454_3.R1040
 5'-most EST zzp700835538.h1

Seq. No. 5819
 Contig ID 5455_1.R1040
 5'-most EST LIB3049-055-Q1-E1-B8
 Method BLASTX
 NCBI GI g3876299
 BLAST score 325
 E value 7.0e-30
 Match length 135
 % identity 48
 NCBI Description (Z71180) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabdi...
 >gi_3880760_emb_CAA16311_ (AL021474) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhab

Seq. No. 5820
 Contig ID 5456_1.R1040
 5'-most EST leu701156483.h1
 Method BLASTX
 NCBI GI g3928090
 BLAST score 318
 E value 2.0e-29
 Match length 104
 % identity 60
 NCBI Description (AC005770) putative MTN3 protein [Arabidopsis thaliana]

Seq. No. 5821
 Contig ID 5458_1.R1040
 5'-most EST zhf700958912.h1
 Method BLASTX
 NCBI GI g3420055
 BLAST score 864
 E value 8.0e-93
 Match length 184
 % identity 88
 NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]

Seq. No. 5822
 Contig ID 5460_1.R1040
 5'-most EST kmv700738102.h1

Seq. No. 5823
 Contig ID 5460_2.R1040
 5'-most EST LIB3051-083-Q1-K1-F6
 Method BLASTX
 NCBI GI g1488647
 BLAST score 2033
 E value 0.0e+00
 Match length 609
 % identity 67
 NCBI Description (X99937) RNA helicase [Spinacia oleracea]

Seq. No. 5824
 Contig ID 5460_3.R1040
 5'-most EST uC-gmropic096e01b1

Seq. No. 5825
 Contig ID 5467_1.R1040
 5'-most EST LIB3049-003-Q1-E1-B10
 Method BLASTN
 NCBI GI g458337
 BLAST score 539
 E value 0.0e+00
 Match length 1127
 % identity 89
 NCBI Description Vigna radiata clone pVR-ACO1
 1-aminocyclopropane-1-carboxylate oxidase homolog mRNA,
 complete cds

Seq. No. 5826
 Contig ID 5467_2.R1040

5'-most EST leu701146339.h1
 Method BLASTN
 NCBI GI g458337
 BLAST score 256
 E value 1.0e-142
 Match length 442
 % identity 90
 NCBI Description Vigna radiata clone pVR-ACO1
 1-aminocyclopropane-1-carboxylate oxidase homolog mRNA,
 complete cds

Seq. No. 5827
 Contig ID 5468_1.R1040
 5'-most EST ssr700555552.h1
 Method BLASTX
 NCBI GI g3785983
 BLAST score 401
 E value 6.0e-39
 Match length 117
 % identity 62
 NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No. 5828
 Contig ID 5469_1.R1040
 5'-most EST jC-gmst02400032b01a1
 Method BLASTX
 NCBI GI g2623296
 BLAST score 677
 E value 4.0e-71
 Match length 232
 % identity 65
 NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No. 5829
 Contig ID 5469_3.R1040
 5'-most EST LIB3106-100-Q1-K1-B8

Seq. No. 5830
 Contig ID 5471_1.R1040
 5'-most EST LIB3051-063-Q1-K1-D9
 Method BLASTX
 NCBI GI g2462762
 BLAST score 959
 E value 1.0e-104
 Match length 288
 % identity 64
 NCBI Description (AC002292) Highly similar to auxin-induced protein
 (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 5831
 Contig ID 5472_1.R1040
 5'-most EST LIB3028-001-Q1-B1-A11
 Method BLASTX
 NCBI GI g4262149
 BLAST score 1131
 E value 1.0e-124
 Match length 268

% identity 73
NCBI Description (AC005275) putative xyloglucan endotransglycosylase
[Arabidopsis thaliana]

Seq. No. 5832
Contig ID 5472_2.R1040
5'-most EST g4260368
Method BLASTX
NCBI GI g4262149
BLAST score 311
E value 2.0e-28
Match length 93
% identity 57
NCBI Description (AC005275) putative xyloglucan endotransglycosylase
[Arabidopsis thaliana]

Seq. No. 5833
Contig ID 5472_3.R1040
5'-most EST zhf700953943.h1
Method BLASTX
NCBI GI g4262149
BLAST score 543
E value 9.0e-56
Match length 170
% identity 59
NCBI Description (AC005275) putative xyloglucan endotransglycosylase
[Arabidopsis thaliana]

Seq. No. 5834
Contig ID 5473_1.R1040
5'-most EST LIB3028-001-Q1-B1-B10
Method BLASTX
NCBI GI g2654559
BLAST score 314
E value 1.0e-28
Match length 152
% identity 39
NCBI Description (AF006621) embryonic lung protein [Homo sapiens]

Seq. No. 5835
Contig ID 5475_1.R1040
5'-most EST zsg701119377.h1

Seq. No. 5836
Contig ID 5480_1.R1040
5'-most EST LIB3028-001-Q1-B1-E10
Method BLASTX
NCBI GI g4539422
BLAST score 581
E value 6.0e-60
Match length 134
% identity 76
NCBI Description (AL049171) putative protein [Arabidopsis thaliana]

Seq. No. 5837
Contig ID 5480_2.R1040
5'-most EST LIB3049-013-Q1-E1-G1

Method BLASTX
 NCBI GI g4539422
 BLAST score 535
 E value 5.0e-55
 Match length 110
 % identity 83
 NCBI Description (AL049171) putative protein [Arabidopsis thaliana]

Seq. No. 5838
 Contig ID 5481_1.R1040
 5'-most EST LIB3028-001-Q1-B1-E12
 Method BLASTX
 NCBI GI g1213629
 BLAST score 771
 E value 4.0e-82
 Match length 238
 % identity 60
 NCBI Description (X95991) pectinesterase [Prunus persica]

Seq. No. 5839
 Contig ID 5482_1.R1040
 5'-most EST jC-gmst02400072a09d1
 Method BLASTX
 NCBI GI g2108252
 BLAST score 317
 E value 3.0e-29
 Match length 102
 % identity 34
 NCBI Description (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
 >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
 (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No. 5840
 Contig ID 5486_1.R1040
 5'-most EST LIB3028-001-Q1-B1-G10
 Method BLASTX
 NCBI GI g132724
 BLAST score 305
 E value 2.0e-27
 Match length 118
 % identity 54
 NCBI Description 50S RIBOSOMAL PROTEIN L18 >gi_71259_pir_R5BS8F ribosomal
 protein L18 - Bacillus stearothermophilus

Seq. No. 5841
 Contig ID 5487_1.R1040
 5'-most EST gsv701056432.h1
 Method BLASTN
 NCBI GI g20866
 BLAST score 196
 E value 1.0e-105
 Match length 585
 % identity 85
 NCBI Description P.sativum mRNA for plastid ribosomal protein CL15

Seq. No. 5842

Contig ID 5487 2.R1040
5'-most EST LIB3028-001-Q1-B1-G11

Seq. No. 5843
Contig ID 5487 3.R1040
5'-most EST pcp700991074.h1
Method BLASTN
NCBI GI g20866
BLAST score 53
E value 4.0e-21
Match length 161
% identity 83
NCBI Description P.sativum mRNA for plastid ribosomal protein CL15

Seq. No. 5844
Contig ID 5497 1.R1040
5'-most EST jC-gmro02910072a11d1
Method BLASTX
NCBI GI g4204294
BLAST score 240
E value 4.0e-20
Match length 82
% identity 62
NCBI Description (AC003027) lcl_prt_seq No definition line found
[Arabidopsis thaliana]

Seq. No. 5845
Contig ID 5498 1.R1040
5'-most EST LIB3049-011-Q1-E1-D3

Seq. No. 5846
Contig ID 5499 1.R1040
5'-most EST LIB3109-056-Q1-K1-E12
Method BLASTX
NCBI GI g1709358
BLAST score 1489
E value 1.0e-166
Match length 441
% identity 64
NCBI Description NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE
PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir_S48859
nucleoside triphosphatase - garden pea
>gi_2129890_pir_S65147 nucleoside triphosphatase
precursor, chromatin-associated - garden pea
>gi_563612_emb_CAA83655_(Z32743) nucleoside triphosphatase
[Pisum sativum] >gi_4519173_dbj_BAA75506.1_(AB022319)
nucleoside triphosphatase (NTPase) [Pisum sativum]

Seq. No. 5847
Contig ID 5501 1.R1040
5'-most EST ncj700975782.h1
Method BLASTX
NCBI GI g2982303
BLAST score 387
E value 2.0e-37
Match length 83
% identity 83

NCBI Description (AF051236) hypothetical protein [Picea mariana]

Seq. No. 5848
Contig ID 5508 1.R1040
5'-most EST LIB3028-005-Q1-B1-C12
Method BLASTX
NCBI GI g2398829
BLAST score 640
E value 1.0e-66
Match length 239
% identity 29
NCBI Description (Y11220) mitochondrial uncoupling protein [Solanum tuberosum]

Seq. No. 5849
Contig ID 5508 2.R1040
5'-most EST LIB3040-031-Q1-E2-H5
Method BLASTX
NCBI GI g2398829
BLAST score 418
E value 7.0e-41
Match length 111
% identity 42
NCBI Description (Y11220) mitochondrial uncoupling protein [Solanum tuberosum]

Seq. No. 5850
Contig ID 5510 1.R1040
5'-most EST LIB3028-005-Q1-B1-D4
Method BLASTX
NCBI GI g2583112
BLAST score 315
E value 9.0e-29
Match length 142
% identity 44
NCBI Description (AC002387) putative PD1-like DNA-binding protein [Arabidopsis thaliana]

Seq. No. 5851
Contig ID 5510 2.R1040
5'-most EST hyd700726712.h1
Method BLASTX
NCBI GI g3668079
BLAST score 177
E value 8.0e-13
Match length 62
% identity 50
NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No. 5852
Contig ID 5512 1.R1040
5'-most EST LIB3092-055-Q1-K1-G10

Seq. No. 5853
Contig ID 5517 1.R1040
5'-most EST LIB3028-006-Q1-B1-D5

BLAST score 1028
 E value 1.0e-112
 Match length 240
 % identity 82
 NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi_542158_pir_S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
 ribosomal protein L7A [Oryza sativa]

Seq. No. 5862
 Contig ID 5536_1.R1040
 5'-most EST asn701135418.h1
 Method BLASTX
 NCBI GI g4234941
 BLAST score 848
 E value 7.0e-99
 Match length 210
 % identity 89
 NCBI Description (AF097938) cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]

Seq. No. 5863
 Contig ID 5540_1.R1040
 5'-most EST jC-gmfl02220094d09a1
 Method BLASTX
 NCBI GI g2102691
 BLAST score 412
 E value 4.0e-40
 Match length 125
 % identity 65
 NCBI Description (U64817) fructokinase [Lycopersicon esculentum]

Seq. No. 5864
 Contig ID 5543_1.R1040
 5'-most EST jC-gmst02400041g07a1
 Method BLASTX
 NCBI GI g123601
 BLAST score 766
 E value 2.0e-81
 Match length 242
 % identity 62
 NCBI Description HEAT SHOCK 70 KD PROTEIN >gi_99913_pir_S14992 heat shock protein, 70K - soybean >gi_18663_emb_CAA44620_ (X62799)
 Heat Shock 70kD protein [Glycine max]

Seq. No. 5865
 Contig ID 5547_1.R1040
 5'-most EST LIB3028-009-Q1-B1-B4
 Method BLASTX
 NCBI GI g2827704
 BLAST score 218
 E value 2.0e-17
 Match length 82
 % identity 54
 NCBI Description (AL021684) LRR-like protein [Arabidopsis thaliana]

Seq. No. 5866
 Contig ID 5548_1.R1040

Match length 157
 % identity 38
 NCBI Description CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) >gi_458230 (U04380) calcineurin B [Naegleria gruberi]

Seq. No. 5883
 Contig ID 5573_1.R1040
 5'-most EST ncj700983528.h1
 Method BLASTX
 NCBI GI g557882
 BLAST score 361
 E value 5.0e-34
 Match length 183
 % identity 45
 NCBI Description (U13923) putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family [Solanum pimpinellifolium] >gi_1809263 (U59317) serine/threonine protein kinase Fen [Lycopersicon pimpinellifolium] >gi_1096880_prf_2112354B Fen gene [Lycopersicon esculentum] >gi_1098334_prf_2115395A Fen gene [Lycopersicon esculentum]

Seq. No. 5884
 Contig ID 5573_2.R1040
 5'-most EST zsq701127563.h1

Seq. No. 5885
 Contig ID 5575_1.R1040
 5'-most EST uC-gmropic090e01b1

Seq. No. 5886
 Contig ID 5576_1.R1040
 5'-most EST zzp700831186.h1
 Method BLASTX
 NCBI GI g2501102
 BLAST score 212
 E value 6.0e-17
 Match length 100
 % identity 49
 NCBI Description SYNTAXIN-RELATED PROTEIN KNOLLE >gi_1184165 (U39451) syntaxin-related [Arabidopsis thaliana] >gi_1184167 (U39452) syntaxin-related [Arabidopsis thaliana] >gi_3063443 (AC003981) F22O13.4 [Arabidopsis thaliana] >gi_1587182_prf_2206310A syntaxin-related protein [Arabidopsis thaliana]

Seq. No. 5887
 Contig ID 5577_1.R1040
 5'-most EST LIB3028-010-Q1-B1-E1
 Method BLASTX
 NCBI GI g4204315
 BLAST score 404
 E value 9.0e-42
 Match length 148
 % identity 59

Seq. No. 5900
Contig ID 5595_1.R1040
5'-most EST LIB3052-007-Q1-B1-A2

Seq. No. 5901
Contig ID 5597_1.R1040
5'-most EST LIB3072-012-Q1-E1-G8
Method BLASTX
NCBI GI g2047324
BLAST score 696
E value 3.0e-73
Match length 157
% identity 78
NCBI Description (U80192) HAL3 homolog [Arabidopsis thaliana]

Seq. No. 5902
Contig ID 5597_2.R1040
5'-most EST LIB3051-028-Q1-K1-D1
Method BLASTX
NCBI GI g4106515
BLAST score 648
E value 1.0e-80
Match length 183
% identity 80
NCBI Description (AF092743) CAK associated cyclinH homolog [Populus tremula x Populus tremuloides]

Seq. No. 5903
Contig ID 5597_3.R1040
5'-most EST LIB3093-058-Q1-K1-A11

Seq. No. 5904
Contig ID 5597_4.R1040
5'-most EST LIB3109-047-Q1-K1-A10

Seq. No. 5905
Contig ID 5597_5.R1040
5'-most EST g5126313

Seq. No. 5906
Contig ID 5597_6.R1040
5'-most EST leu701147304.h1

Seq. No. 5907
Contig ID 5597_7.R1040
5'-most EST LIB3093-012-Q1-K1-D9
Method BLASTX
NCBI GI g549706
BLAST score 193
E value 2.0e-14
Match length 113
% identity 36
NCBI Description KTI12 PROTEIN >gi_539197_pir_S37937 KTI12 protein - yeast (Saccharomyces cerevisiae) >gi_486185_emb_CAA81950_ (Z28110) ORF YKL110c [Saccharomyces cerevisiae] >gi_536816_emb_CAA54646_ (X77511) KTI12 [Saccharomyces cerevisiae]

Seq. No.	5908
Contig ID	5597_8.R1040
5'-most EST	yya700764032.h1
Seq. No.	5909
Contig ID	5597_9.R1040
5'-most EST	zsg701129470.h1
Method	BLASTN
NCBI GI	g4519195
BLAST score	36
E value	2.0e-10
Match length	172
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence
Seq. No.	5910
Contig ID	5597_11.R1040
5'-most EST	LIB3050-020-Q1-K1-C4
Seq. No.	5911
Contig ID	5597_12.R1040
5'-most EST	uC-gmrominsoy201a07b1
Seq. No.	5912
Contig ID	5597_14.R1040
5'-most EST	uaw700661065.h1
Seq. No.	5913
Contig ID	5597_20.R1040
5'-most EST	dpv701098531.h1
Seq. No.	5914
Contig ID	5597_21.R1040
5'-most EST	ncj700979023.h1
Seq. No.	5915
Contig ID	5603_1.R1040
5'-most EST	gsv701055160.h1
Seq. No.	5916
Contig ID	5605_1.R1040
5'-most EST	LIB3028-012-Q1-B1-A1
Seq. No.	5917
Contig ID	5608_1.R1040
5'-most EST	ncj700981742.h1
Method	BLASTX
NCBI GI	g2497702
BLAST score	137
E value	8.0e-15
Match length	118
% identity	47
NCBI Description	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi_2121019_pir_I40710 outer membrane lipoprotein - Citrobacter freundii >gi_717136 (U21727) lipocalin

[illegible][illegible][illegible][illegible][illegible][illegible][illegible]

06-07-2018

[illegible]

Contig ID 5679_3.R1040
5'-most EST leu701150389.h1

Seq. No. 5963
Contig ID 5680_1.R1040
5'-most EST ssr700554933.h1

Seq. No. 5964
Contig ID 5684_1.R1040
5'-most EST LIB3030-009-Q1-B1-H11
Method BLASTX
NCBI GI g2914700
BLAST score 786
E value 1.0e-83
Match length 277
% identity 61
NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No. 5965
Contig ID 5685_1.R1040
5'-most EST LIB3170-070-Q1-J1-H10

Seq. No. 5966
Contig ID 5686_1.R1040
5'-most EST txt700736063.h1
Method BLASTX
NCBI GI g118507
BLAST score 699
E value 2.0e-73
Match length 309
% identity 46
NCBI Description ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (CLASS 3) (TUMOR-ASSOCIATED ALDEHYDE DEHYDROGENASE) (HTC-ALDH) >gi_91936_pir_A30149 aldehyde dehydrogenase (NADP+) (EC 1.2.1.4) 3, tumor-associated - rat >gi_202833 (J03637) aldehyde dehydrogenase [Rattus norvegicus]

Seq. No. 5967
Contig ID 5688_1.R1040
5'-most EST LIB3028-021-Q1-B1-H4

Seq. No. 5968
Contig ID 5696_1.R1040
5'-most EST leu701152149.h1
Method BLASTX
NCBI GI g2739044
BLAST score 1226
E value 1.0e-135
Match length 321
% identity 70
NCBI Description (AF024651) polyphosphoinositide binding protein Sshlp [Glycine max]

Seq. No. 5969
Contig ID 5696_2.R1040
5'-most EST g5753550

Method BLASTX
 NCBI GI g2739044
 BLAST score 373
 E value 1.0e-35
 Match length 108
 % identity 65
 NCBI Description (AF024651) polyphosphoinositide binding protein Sshlp
 [Glycine max]

Seq. No. 5970
 Contig ID 5697_1.R1040
 5'-most EST vwf700678766.h1

Seq. No. 5971
 Contig ID 5698_1.R1040
 5'-most EST LIB3049-019-Q1-E1-A6
 Method BLASTX
 NCBI GI g1001607
 BLAST score 290
 E value 2.0e-25
 Match length 136
 % identity 39
 NCBI Description (D64000) hypothetical protein [Synechocystis sp.]

Seq. No. 5972
 Contig ID 5698_2.R1040
 5'-most EST LIB3139-033-P1-N1-D8

Seq. No. 5973
 Contig ID 5700_1.R1040
 5'-most EST LIB3028-023-Q1-B1-E8

Seq. No. 5974
 Contig ID 5704_1.R1040
 5'-most EST LIB3056-009-Q1-N1-B6
 Method BLASTX
 NCBI GI g1916613
 BLAST score 232
 E value 8.0e-19
 Match length 175
 % identity 37
 NCBI Description (U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]

Seq. No. 5975
 Contig ID 5710_1.R1040
 5'-most EST LIB3028-025-Q1-B1-B11

Seq. No. 5976
 Contig ID 5718_1.R1040
 5'-most EST jC-gmf102220130d06d1

Seq. No. 5977
 Contig ID 5729_1.R1040
 5'-most EST fde700876539.h1
 Method BLASTX
 NCBI GI g2271477
 BLAST score 431

E value 2.0e-42
 Match length 85
 % identity 95
 NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No. 5978
 Contig ID 5732_1.R1040
 5'-most EST LIB3170-042-Q1-J1-C10
 Method BLASTN
 NCBI GI g4263694
 BLAST score 51
 E value 9.0e-20
 Match length 135
 % identity 84
 NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 5979
 Contig ID 5732_2.R1040
 5'-most EST taw700658026.h1
 Method BLASTX
 NCBI GI g4263711
 BLAST score 522
 E value 3.0e-53
 Match length 114
 % identity 84
 NCBI Description (AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No. 5980
 Contig ID 5735_1.R1040
 5'-most EST wvk700683896.h1
 Method BLASTX
 NCBI GI g1076579
 BLAST score 676
 E value 3.0e-71
 Match length 167
 % identity 75
 NCBI Description alcohol dehydrogenase homolog ADH3a - tomato

Seq. No. 5981
 Contig ID 5736_1.R1040
 5'-most EST dpv701102630.h1
 Method BLASTX
 NCBI GI g2245127
 BLAST score 166
 E value 1.0e-11
 Match length 74
 % identity 47
 NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 5982
 Contig ID 5740_1.R1040
 5'-most EST vwf700676662.h1

Seq. No. 5983
 Contig ID 5752_1.R1040

5'-most EST	LIB3170-076-Q1-J1-A10
Seq. No.	5984
Contig ID	5755_1.R1040
5'-most EST	uC-gmflminsoy076f04b1
Method	BLASTX
NCBI GI	g4508068
BLAST score	250
E value	1.0e-20
Match length	151
% identity	42
NCBI Description	(AC005882) 3063 [Arabidopsis thaliana]
Seq. No.	5985
Contig ID	5756_1.R1040
5'-most EST	jC-gmfl02220075f08d1
Method	BLASTN
NCBI GI	g1841474
BLAST score	38
E value	6.0e-12
Match length	64
% identity	91
NCBI Description	P.sativum mRNA for Myb-like protein (Myb26)
Seq. No.	5986
Contig ID	5763_1.R1040
5'-most EST	LIB3028-039-Q1-B1-B5
Seq. No.	5987
Contig ID	5763_2.R1040
5'-most EST	LIB3107-080-Q1-K1-D1
Seq. No.	5988
Contig ID	5763_3.R1040
5'-most EST	uC-gmrominsoy115g03b1
Seq. No.	5989
Contig ID	5777_1.R1040
5'-most EST	LIB3028-040-Q1-B1-H4
Method	BLASTX
NCBI GI	g4490752
BLAST score	580
E value	8.0e-60
Match length	134
% identity	78
NCBI Description	(AL035708) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	5990
Contig ID	5780_1.R1040
5'-most EST	uC-gmronoir015c09b1
Method	BLASTX
NCBI GI	g4512625
BLAST score	293
E value	5.0e-26
Match length	236
% identity	32

NCBI Description (AC004793) ESTs gb_T20423, gb_AA712864, gb_H76323 and gb_Z25560 come from this gene. [Arabidopsis thaliana]

Seq. No. 5991
 Contig ID 5784_1.R1040
 5'-most EST LIB3028-041-Q1-B1-F12
 Method BLASTX
 NCBI GI g3258637
 BLAST score 537
 E value 7.0e-55
 Match length 145
 % identity 70
 NCBI Description (AF041050) 4-coumarate:CoA ligase [Populus tremuloides]

Seq. No. 5992
 Contig ID 5786_1.R1040
 5'-most EST zpv700763688.h1

Seq. No. 5993
 Contig ID 5787_1.R1040
 5'-most EST trc700562171.h1
 Method BLASTX
 NCBI GI g4544389
 BLAST score 708
 E value 2.0e-74
 Match length 381
 % identity 46
 NCBI Description (AC007047) putative homeodomain protein [Arabidopsis thaliana]

Seq. No. 5994
 Contig ID 5791_1.R1040
 5'-most EST zzp700832642.h1
 Method BLASTX
 NCBI GI g1085002
 BLAST score 552
 E value 4.0e-56
 Match length 295
 % identity 42
 NCBI Description mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans >gi_472902_emb_CAA53721_ (X76115) carrier protein (c1) [Caenorhabditis elegans] >gi_829102_emb_CAA88283_ (Z48240) DIF-1 [Caenorhabditis elegans]

Seq. No. 5995
 Contig ID 5791_2.R1040
 5'-most EST LIB3107-061-Q1-K1-G9
 Method BLASTX
 NCBI GI g1085002
 BLAST score 179
 E value 6.0e-13
 Match length 58
 % identity 53
 NCBI Description mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans >gi_472902_emb_CAA53721_ (X76115) carrier protein (c1) [Caenorhabditis elegans]

09684016.101000

>gi_829102_emb_CAA88283_ (Z48240) DIF-1 [Caenorhabditis elegans]

Seq. No. 5996
Contig ID 5791_4.R1040
5'-most EST rlr700895682.h1

Seq. No. 5997
Contig ID 5791_5.R1040
5'-most EST bth700849349.h1

Seq. No. 5998
Contig ID 5792_1.R1040
5'-most EST LIB3028-042-Q1-B1-H12

Seq. No. 5999
Contig ID 5795_1.R1040
5'-most EST ssr700555019.h1

Seq. No. 6000
Contig ID 5797_1.R1040
5'-most EST hyd700726496.h1
Method BLASTX
NCBI GI g3831441
BLAST score 179
E value 3.0e-12
Match length 47
% identity 87
NCBI Description (AC005819) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6001
Contig ID 5797_2.R1040
5'-most EST jC-gmf102220073f08d1

Seq. No. 6002
Contig ID 5798_1.R1040
5'-most EST g4291359
Method BLASTX
NCBI GI g3335375
BLAST score 222
E value 1.0e-17
Match length 89
% identity 44
NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]

Seq. No. 6003
Contig ID 5804_1.R1040
5'-most EST LIB3074-028-Q1-K1-F10
Method BLASTX
NCBI GI g4104816
BLAST score 505
E value 6.0e-51
Match length 136
% identity 70
NCBI Description (AF039662) ferredoxin-like protein [Capsicum annuum]

Seq. No. 6004

Contig ID	5804_2.R1040
5'-most EST	LIB3106-014-Q1-K1-B6
Method	BLASTX
NCBI GI	g4104816
BLAST score	473
E value	2.0e-47
Match length	130
% identity	68
NCBI Description	(AF039662) ferredoxin-like protein [Capsicum annuum]
Seq. No.	6005
Contig ID	5804_3.R1040
5'-most EST	LIB3106-092-Q1-K1-B12
Method	BLASTX
NCBI GI	g3023752
BLAST score	437
E value	3.0e-43
Match length	114
% identity	71
NCBI Description	FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520) ferredoxin-I [Lycopersicon esculentum]
Seq. No.	6006
Contig ID	5804_4.R1040
5'-most EST	LIB3093-006-Q1-K1-A2
Method	BLASTX
NCBI GI	g1834353
BLAST score	213
E value	9.0e-17
Match length	67
% identity	57
NCBI Description	(Y10986) hypothetical protein 194 [Arabidopsis thaliana]
Seq. No.	6007
Contig ID	5804_6.R1040
5'-most EST	LIB3051-014-Q1-E1-F9
Method	BLASTX
NCBI GI	g1834353
BLAST score	215
E value	6.0e-17
Match length	245
% identity	29
NCBI Description	(Y10986) hypothetical protein 194 [Arabidopsis thaliana]
Seq. No.	6008
Contig ID	5808_1.R1040
5'-most EST	LIB3028-045-Q1-B1-D2
Seq. No.	6009
Contig ID	5809_1.R1040
5'-most EST	LIB3092-037-Q1-K1-D11
Method	BLASTX
NCBI GI	g2829897
BLAST score	201
E value	3.0e-15
Match length	141
% identity	31

NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No. 6010
Contig ID 5809_2.R1040
5'-most EST uxk700670728.h1

Seq. No. 6011
Contig ID 5809_3.R1040
5'-most EST LIB3107-063-Q1-K1-D6
Method BLASTX
NCBI GI g2829897
BLAST score 273
E value 8.0e-24
Match length 91
% identity 66

NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No. 6012
Contig ID 5811_1.R1040
5'-most EST jC-gmst02400065e04a2
Method BLASTX
NCBI GI g3288809
BLAST score 259
E value 9.0e-22
Match length 150
% identity 43

NCBI Description (AF013169) beta-glucosidase [Pyrococcus furiosus]

Seq. No. 6013
Contig ID 5812_1.R1040
5'-most EST jC-gmle01810021e01d1
Method BLASTX
NCBI GI g3142294
BLAST score 423
E value 2.0e-41
Match length 93
% identity 87

NCBI Description (AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No. 6014
Contig ID 5816_1.R1040
5'-most EST jC-gmf102220056b06d1

Seq. No. 6015
Contig ID 5818_1.R1040
5'-most EST ncj700980756.h1

Seq. No. 6016
Contig ID 5819_1.R1040
5'-most EST LIB3028-047-Q1-B1-A9

Seq. No. 6017
Contig ID 5822_2.R1040
5'-most EST LIB3039-052-Q1-E1-H8
Method BLASTX

5'-most EST ssr700557855.h1

Seq. No. 6036
 Contig ID 5874_1.R1040
 5'-most EST LIB3087-001-Q1-K1-D3
 Method BLASTX
 NCBI GI g2435511
 BLAST score 337
 E value 2.0e-31
 Match length 111
 % identity 57
 NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase
 alpha subunit [Arabidopsis thaliana]

Seq. No. 6037
 Contig ID 5877_1.R1040
 5'-most EST jC-gmle01810087g09a1
 Method BLASTN
 NCBI GI g2924257
 BLAST score 154
 E value 2.0e-80
 Match length 541
 % identity 91
 NCBI Description Tobacco chloroplast genome DNA

Seq. No. 6038
 Contig ID 5877_2.R1040
 5'-most EST awf700838734.h1
 Method BLASTN
 NCBI GI g2924257
 BLAST score 146
 E value 4.0e-76
 Match length 380
 % identity 84
 NCBI Description Tobacco chloroplast genome DNA

Seq. No. 6039
 Contig ID 5877_3.R1040
 5'-most EST fde700872365.h1
 Method BLASTN
 NCBI GI g1143165
 BLAST score 196
 E value 1.0e-106
 Match length 430
 % identity 86
 NCBI Description Nicotiana tabacum ClpP protease (ClpP) mRNA, chloroplast
 gene encoding chloroplast protein, complete cds

Seq. No. 6040
 Contig ID 5878_1.R1040
 5'-most EST epx701107225.h1
 Method BLASTN
 NCBI GI g18662
 BLAST score 359
 E value 0.0e+00
 Match length 374
 % identity 99

NCBI Description Glycine max hsp 70 gene

Seq. No. 6041
Contig ID 5893_1.R1040
5'-most EST LIB3029-012-Q1-B1-D8

Seq. No. 6042
Contig ID 5895_1.R1040
5'-most EST fC-gmst700837068d1

Seq. No. 6043
Contig ID 5899_1.R1040
5'-most EST LIB3029-003-Q1-B1-H1
Method BLASTX
NCBI GI g4432827
BLAST score 247
E value 9.0e-21
Match length 176
% identity 36
NCBI Description (AC006593) putative ADP-ribose polymerase [Arabidopsis thaliana]

Seq. No. 6044
Contig ID 5900_1.R1040
5'-most EST uC-gmrominsoy065f11b1
Method BLASTX
NCBI GI g1685005
BLAST score 296
E value 1.0e-26
Match length 121
% identity 46
NCBI Description (U32644) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

Seq. No. 6045
Contig ID 5906_1.R1040
5'-most EST jC-gmst02400029h05a1
Method BLASTX
NCBI GI g1707412
BLAST score 884
E value 5.0e-95
Match length 417
% identity 44
NCBI Description (X95906) Cleavage and Polyadenylation Specificity Factor protein [Bos taurus]

Seq. No. 6046
Contig ID 5917_1.R1040
5'-most EST zsg701126164.h1

Seq. No. 6047
Contig ID 5917_2.R1040
5'-most EST LIB3029-011-Q1-B1-H5

Seq. No. 6048
Contig ID 5925_1.R1040
5'-most EST LIB3029-012-Q1-B1-A6

09684016-101000

Seq. No. 6049
Contig ID 5925_2.R1040
5'-most EST awf700836732.h1
Method BLASTN
NCBI GI g170005
BLAST score 75
E value 6.0e-34
Match length 91
% identity 96
NCBI Description Soybean lectin (Lel) gene, complete cds

Seq. No. 6050
Contig ID 5927_1.R1040
5'-most EST uC-gmropic106c06b1
Method BLASTN
NCBI GI g1177602
BLAST score 576
E value 0.0e+00
Match length 1016
% identity 89
NCBI Description P.sativum mRNA for pyruvate decarboxylase (PDC1)

Seq. No. 6051
Contig ID 5927_2.R1040
5'-most EST uC-gmropic088b10b1
Method BLASTN
NCBI GI g1177602
BLAST score 322
E value 0.0e+00
Match length 693
% identity 90
NCBI Description P.sativum mRNA for pyruvate decarboxylase (PDC1)

Seq. No. 6052
Contig ID 5930_1.R1040
5'-most EST LIB3050-021-Q1-K1-B8
Method BLASTX
NCBI GI g3399767
BLAST score 160
E value 1.0e-10
Match length 112
% identity 29
NCBI Description (U76298) uclacyanin I [Arabidopsis thaliana] >gi_3831466
(AC005700) uclacyanin I [Arabidopsis thaliana]

Seq. No. 6053
Contig ID 5930_2.R1040
5'-most EST LIB3109-009-Q1-K1-C1

Seq. No. 6054
Contig ID 5933_1.R1040
5'-most EST LIB3049-022-Q1-E1-G11
Method BLASTX
NCBI GI g1352681
BLAST score 648
E value 1.0e-67

Seq. No. 6061
 Contig ID 5937_1.R1040
 5'-most EST leu701144592.h1
 Method BLASTX
 NCBI GI g3687250
 BLAST score 907
 E value 5.0e-98
 Match length 208
 % identity 80
 NCBI Description (AC005169) putative arginine n-methyltransferase
 [Arabidopsis thaliana]

Seq. No. 6062
 Contig ID 5938_1.R1040
 5'-most EST uC-gmflminsoy047g04b1
 Method BLASTX
 NCBI GI g130720
 BLAST score 289
 E value 8.0e-26
 Match length 112
 % identity 48
 NCBI Description PROTEOLIPID PROTEIN PPA1 >gi_101508_pir_A34633 probable
 H⁺-transporting ATPase (EC 3.6.1.35) lipid-binding protein
 - yeast (Saccharomyces cerevisiae) >gi_172221 (M35294)
 proteolipid protein of proton ATPase [Saccharomyces
 cerevisiae] >gi_500700 (U10399) Ppalp: Proteolipid protein
 of proton ATPase [Saccharomyces cerevisiae]

Seq. No. 6063
 Contig ID 5938_2.R1040
 5'-most EST g5605673
 Method BLASTX
 NCBI GI g130720
 BLAST score 267
 E value 4.0e-23
 Match length 108
 % identity 61
 NCBI Description PROTEOLIPID PROTEIN PPA1 >gi_101508_pir_A34633 probable
 H⁺-transporting ATPase (EC 3.6.1.35) lipid-binding protein
 - yeast (Saccharomyces cerevisiae) >gi_172221 (M35294)
 proteolipid protein of proton ATPase [Saccharomyces
 cerevisiae] >gi_500700 (U10399) Ppalp: Proteolipid protein
 of proton ATPase [Saccharomyces cerevisiae]

Seq. No. 6064
 Contig ID 5951_1.R1040
 5'-most EST sat701008670.h1
 Method BLASTX
 NCBI GI g1174448
 BLAST score 599
 E value 7.0e-62
 Match length 222
 % identity 54
 NCBI Description TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR
 (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)
 (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative

(Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
 >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
 [Arabidopsis thaliana]

Seq. No. 6070
 Contig ID 5958_3.R1040
 5'-most EST leu701151437.h1
 Method BLASTX
 NCBI GI g4115925
 BLAST score 280
 E value 2.0e-24
 Match length 126
 % identity 52
 NCBI Description (AF118222) contains similarity to RNA recognition motifs
 (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
 >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
 [Arabidopsis thaliana]

Seq. No. 6071
 Contig ID 5958_4.R1040
 5'-most EST vzy700755441.h1

Seq. No. 6072
 Contig ID 5958_5.R1040
 5'-most EST gsv701048154.h1

Seq. No. 6073
 Contig ID 5960_1.R1040
 5'-most EST ncj700984222.h1
 Method BLASTX
 NCBI GI g118926
 BLAST score 709
 E value 7.0e-75
 Match length 201
 % identity 67
 NCBI Description DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
 >gi_320600_pir_E45509 desiccation-related protein (clone
 PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991)
 dessication-related protein [Craterostigma plantagineum]
 >gi_227781_prf_1710351E abscisic acid responsive protein E
 [Craterostigma plantagineum]

Seq. No. 6074
 Contig ID 5966_1.R1040
 5'-most EST smc700750004.h1
 Method BLASTX
 NCBI GI g542190
 BLAST score 613
 E value 2.0e-63
 Match length 287
 % identity 45
 NCBI Description hypothetical protein 1087 - maize >gi_459269_emb_CAA54960_
 (X78029) transcribed sequence 1087 [Zea mays]

Seq. No. 6075
 Contig ID 5966_2.R1040
 5'-most EST smc700745314.h1

Match length 151
 % identity 87
 NCBI Description PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)
 (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)
 >gi_2285802_dbj_BAA21651_ (D78173) 26S proteasome alpha
 subunit [*Spinacia oleracea*]

Seq. No. 6081
 Contig ID 5983_1.R1040
 5'-most EST leu701146005.h1
 Method BLASTX
 NCBI GI g2660676
 BLAST score 811
 E value 1.0e-86
 Match length 206
 % identity 73
 NCBI Description (AC002342) Dreg-2 like protein [*Arabidopsis thaliana*]

Seq. No. 6082
 Contig ID 5985_1.R1040
 5'-most EST awf700840391.h1
 Method BLASTX
 NCBI GI g81886
 BLAST score 753
 E value 6.0e-80
 Match length 205
 % identity 71
 NCBI Description tonoplast intrinsic protein alpha - kidney bean

Seq. No. 6083
 Contig ID 5987_1.R1040
 5'-most EST zhf700952328.h1

Seq. No. 6084
 Contig ID 5987_2.R1040
 5'-most EST jC-gmf102220114f01a1

Seq. No. 6085
 Contig ID 5994_1.R1040
 5'-most EST crh700853990.h1
 Method BLASTX
 NCBI GI g2245066
 BLAST score 1398
 E value 1.0e-155
 Match length 460
 % identity 58
 NCBI Description (Z97342) Beta-Amylase [*Arabidopsis thaliana*]

Seq. No. 6086
 Contig ID 5994_2.R1040
 5'-most EST rca700996317.h1
 Method BLASTX
 NCBI GI g2245066
 BLAST score 259
 E value 2.0e-22
 Match length 128
 % identity 45

E value 3.0e-37
 Match length 141
 % identity 54
 NCBI Description (AL022605) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6095
 Contig ID 6007_1.R1040
 5'-most EST LIB3029-010-Q1-B1-B7
 Method BLASTX
 NCBI GI g2652938
 BLAST score 902
 E value 1.0e-97
 Match length 190
 % identity 87
 NCBI Description (Z47554) orf [Zea mays]

Seq. No. 6096
 Contig ID 6011_1.R1040
 5'-most EST uaw700661589.h1
 Method BLASTX
 NCBI GI g126078
 BLAST score 510
 E value 1.0e-51
 Match length 184
 % identity 62
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)
 >gi_81554_pir_S04046 embryonic abundant protein gD-34 -
 upland cotton >gi_18501_emb_CAA31594 (X13206) D-34 Lea
 protein [Gossypium hirsutum] >gi_167385 (M19389) storage
 protein [Gossypium hirsutum] >gi_226556_prf_1601521F Lea
 D-34 gene [Saguinus oedipus]

Seq. No. 6097
 Contig ID 6013_1.R1040
 5'-most EST LIB3029-010-Q1-B1-A5

Seq. No. 6098
 Contig ID 6016_1.R1040
 5'-most EST LIB3029-010-Q1-B1-A8
 Method BLASTX
 NCBI GI g4510383
 BLAST score 559
 E value 2.0e-57
 Match length 190
 % identity 64
 NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 6099
 Contig ID 6018_1.R1040
 5'-most EST LIB3051-010-Q1-E1-G10
 Method BLASTX
 NCBI GI g3080439
 BLAST score 151
 E value 9.0e-10
 Match length 75
 % identity 44
 NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

% identity 90
 NCBI Description Phaseolus vulgaris putative osmoprotector PvLEA-18
 (Pvlea-18) mRNA, complete cds

Seq. No. 6113
 Contig ID 6048_1.R1040
 5'-most EST leu701156292.h1
 Method BLASTX
 NCBI GI g4337179
 BLAST score 314
 E value 9.0e-29
 Match length 145
 % identity 49
 NCBI Description (AC006416) This gene is continued on the 5' end of BAC
 T12M14. [Arabidopsis thaliana]

Seq. No. 6114
 Contig ID 6049_1.R1040
 5'-most EST jC-gmfl02220108f01a1
 Method BLASTX
 NCBI GI g2618705
 BLAST score 876
 E value 2.0e-94
 Match length 271
 % identity 68
 NCBI Description (AC002510) putative ABC transporter, 5' partial
 [Arabidopsis thaliana]

Seq. No. 6115
 Contig ID 6072_1.R1040
 5'-most EST gsv701046930.h1
 Method BLASTX
 NCBI GI g2342727
 BLAST score 281
 E value 5.0e-25
 Match length 68
 % identity 71
 NCBI Description (AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6116
 Contig ID 6075_1.R1040
 5'-most EST has700548234.h1
 Method BLASTX
 NCBI GI g2956717
 BLAST score 237
 E value 8.0e-20
 Match length 125
 % identity 46
 NCBI Description (Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]

Seq. No. 6117
 Contig ID 6078_1.R1040
 5'-most EST LIB3029-008-Q1-B1-G2

Seq. No. 6118
 Contig ID 6080_1.R1040
 5'-most EST epx701106595.h1

09684016.101000

Method BLASTX
 NCBI GI g2842757
 BLAST score 192
 E value 3.0e-14
 Match length 109
 % identity 43
 NCBI Description LIGHT-INDUCIBLE PROTEIN CPRF-2 >gi_1806261_emb_CAA41453_ (X58577) DNA-binding protein; bZIP type [Petroselinum crispum]

Seq. No. 6119
 Contig ID 6080_2.R1040
 5'-most EST jC-gmfl02220102e09a1
 Method BLASTX
 NCBI GI g2842757
 BLAST score 245
 E value 2.0e-21
 Match length 156
 % identity 46
 NCBI Description LIGHT-INDUCIBLE PROTEIN CPRF-2 >gi_1806261_emb_CAA41453_ (X58577) DNA-binding protein; bZIP type [Petroselinum crispum]

Seq. No. 6120
 Contig ID 6080_3.R1040
 5'-most EST uC-gmropic113g07b1
 Method BLASTX
 NCBI GI g100163
 BLAST score 230
 E value 6.0e-19
 Match length 147
 % identity 40
 NCBI Description light-induced protein CPRF-2 - parsley

Seq. No. 6121
 Contig ID 6082_1.R1040
 5'-most EST pcp700990468.h1
 Method BLASTX
 NCBI GI g1914683
 BLAST score 905
 E value 1.0e-97
 Match length 245
 % identity 74
 NCBI Description (Y12013) RAD23, isoform I [Daucus carota]

Seq. No. 6122
 Contig ID 6082_2.R1040
 5'-most EST LIB3093-001-Q1-K1-G12
 Method BLASTX
 NCBI GI g1914683
 BLAST score 413
 E value 3.0e-40
 Match length 107
 % identity 78
 NCBI Description (Y12013) RAD23, isoform I [Daucus carota]

Seq. No. 6123

Contig ID 6082_3.R1040
 5'-most EST crh700852624.h1
 Method BLASTX
 NCBI GI g1914683
 BLAST score 289
 E value 7.0e-26
 Match length 74
 % identity 76
 NCBI Description (Y12013) RAD23, isoform I [Daucus carota]

Seq. No. 6124
 Contig ID 6087_1.R1040
 5'-most EST LIB3029-008-Q1-B1-D3
 Method BLASTX
 NCBI GI g130718
 BLAST score 338
 E value 1.0e-31
 Match length 100
 % identity 61
 NCBI Description ACID PHOSPHATASE PRECURSOR 1 >gi_170370 (M83211) acid
 phosphatase type 1 [Lycopersicon esculentum] >gi_170372
 (M67474) acid phosphatase type 5 [Lycopersicon esculentum]
 >gi_445121_prf__1908427A acid phosphatase 1 [Lycopersicon
 esculentum]

Seq. No. 6125
 Contig ID 6089_1.R1040
 5'-most EST LIB3087-008-Q1-K1-A6

Seq. No. 6126
 Contig ID 6089_2.R1040
 5'-most EST LIB3139-013-P1-N1-G7

Seq. No. 6127
 Contig ID 6095_1.R1040
 5'-most EST jC-gmf102220108h05a1
 Method BLASTX
 NCBI GI g4325342
 BLAST score 548
 E value 5.0e-56
 Match length 240
 % identity 53
 NCBI Description (AF128393) No definition line found [Arabidopsis thaliana]

Seq. No. 6128
 Contig ID 6102_1.R1040
 5'-most EST LIB3170-064-Q1-J1-E9

Seq. No. 6129
 Contig ID 6102_2.R1040
 5'-most EST jC-gmf102220057h09d1
 Method BLASTX
 NCBI GI g1171866
 BLAST score 273
 E value 6.0e-24
 Match length 52
 % identity 94

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
(COMPLEX I-20KD) (CI-20KD) >gi_629601_pir_S48826 NADH
dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild
cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of
NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No. 6130
Contig ID 6106_1.R1040
5'-most EST pmv700893391.h1
Method BLASTN
NCBI GI g1161251
BLAST score 61
E value 2.0e-25
Match length 253
% identity 81
NCBI Description Glycine max nucleosome assembly protein 1 (SNAP-1) mRNA,
complete cds

Seq. No. 6131
Contig ID 6112_1.R1040
5'-most EST gsv701055056.h1
Method BLASTX
NCBI GI g3261634
BLAST score 187
E value 1.0e-13
Match length 190
% identity 32
NCBI Description (Z79700) hypothetical protein Rv0976c [Mycobacterium
tuberculosis]

Seq. No. 6132
Contig ID 6114_1.R1040
5'-most EST LIB3029-008-Q1-B1-D1
Method BLASTX
NCBI GI g3914002
BLAST score 923
E value 1.0e-100
Match length 189
% identity 93
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279
(AF033862) Lon protease [Arabidopsis thaliana]

Seq. No. 6133
Contig ID 6115_1.R1040
5'-most EST LIB3107-016-Q1-K1-D3
Method BLASTX
NCBI GI g4371285
BLAST score 171
E value 4.0e-12
Match length 63
% identity 54
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6134
Contig ID 6116_1.R1040
5'-most EST epv701108611.h1

09684015.101000

Seq. No. 6135
Contig ID 6118_1.R1040
5'-most EST LIB3139-103-P1-N1-A9

Seq. No. 6136
Contig ID 6118_2.R1040
5'-most EST g5058185

Seq. No. 6137
Contig ID 6120_1.R1040
5'-most EST LIB3029-007-Q1-B1-H7

Seq. No. 6138
Contig ID 6121_1.R1040
5'-most EST LIB3029-008-Q1-B1-A11

Seq. No. 6139
Contig ID 6126_1.R1040
5'-most EST zzp700832478.h1
Method BLASTX
NCBI GI g3482967
BLAST score 758
E value 1.0e-149
Match length 359
% identity 72
NCBI Description (AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 6140
Contig ID 6127_1.R1040
5'-most EST LIB3167-042-P1-K1-H4
Method BLASTX
NCBI GI g2078350
BLAST score 721
E value 2.0e-76
Match length 199
% identity 70
NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 6141
Contig ID 6127_2.R1040
5'-most EST leu701152348.h1
Method BLASTX
NCBI GI g2078350
BLAST score 529
E value 6.0e-54
Match length 136
% identity 71
NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 6142
Contig ID 6129_1.R1040
5'-most EST LIB3029-008-Q1-B1-B2

Seq. No. 6143
Contig ID 6133_1.R1040

09684016-101000

5'-most EST sat701006002.h2
 Method BLASTX
 NCBI GI g2244939
 BLAST score 346
 E value 6.0e-32
 Match length 304
 % identity 31
 NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6144
 Contig ID 6133_2.R1040
 5'-most EST jC-gmle01810044h11d1

Seq. No. 6145
 Contig ID 6133_3.R1040
 5'-most EST vzy700756777.h1

Seq. No. 6146
 Contig ID 6136_1.R1040
 5'-most EST asn701133071.h1
 Method BLASTN
 NCBI GI g18729
 BLAST score 64
 E value 2.0e-27
 Match length 68
 % identity 99
 NCBI Description Soybean (Glycine max) 18S ribosomal RNA

Seq. No. 6147
 Contig ID 6136_2.R1040
 5'-most EST sat701008527.h1
 Method BLASTN
 NCBI GI g18729
 BLAST score 269
 E value 1.0e-149
 Match length 458
 % identity 90
 NCBI Description Soybean (Glycine max) 18S ribosomal RNA

Seq. No. 6148
 Contig ID 6144_1.R1040
 5'-most EST leu701157711.h1
 Method BLASTX
 NCBI GI g2623297
 BLAST score 143
 E value 1.0e-08
 Match length 49
 % identity 55
 NCBI Description (AC002409) unknown protein [Arabidopsis thaliana]
 >gi_3790583 (AF079180) RING-H2 finger protein RHC1a
 [Arabidopsis thaliana]

Seq. No. 6149
 Contig ID 6144_2.R1040
 5'-most EST jC-gmfl02220063c05a1

Seq. No. 6150

Contig ID 6145_1.R1040
 5'-most EST LIB3167-027-P1-K1-A6
 Method BLASTX
 NCBI GI g2462834
 BLAST score 364
 E value 2.0e-34
 Match length 182
 % identity 43
 NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6151
 Contig ID 6145_3.R1040
 5'-most EST wvk700684271.h1
 Method BLASTX
 NCBI GI g3337357
 BLAST score 165
 E value 5.0e-13
 Match length 68
 % identity 62
 NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6152
 Contig ID 6145_4.R1040
 5'-most EST jex700906373.h1
 Method BLASTX
 NCBI GI g3337357
 BLAST score 278
 E value 5.0e-25
 Match length 86
 % identity 65
 NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6153
 Contig ID 6150_1.R1040
 5'-most EST zsg701121114.h1

Seq. No. 6154
 Contig ID 6158_1.R1040
 5'-most EST LIB3029-007-Q1-B1-E9

Seq. No. 6155
 Contig ID 6159_1.R1040
 5'-most EST LIB3029-007-Q1-B1-D3
 Method BLASTX
 NCBI GI g2204234
 BLAST score 485
 E value 4.0e-49
 Match length 118
 % identity 81
 NCBI Description (Y13862) enoyl-ACP reductase [Nicotiana tabacum]

Seq. No. 6156
 Contig ID 6160_1.R1040
 5'-most EST uaw700661722.h1
 Method BLASTX
 NCBI GI g3264830
 BLAST score 212

E value 1.0e-157
 Match length 302
 % identity 82
 NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No. 6164
 Contig ID 6196_1.R1040
 5'-most EST vzy700754476.h1
 Method BLASTX
 NCBI GI g2407613
 BLAST score 705
 E value 8.0e-74
 Match length 442
 % identity 40
 NCBI Description (AF017995) 3-phosphoinositide dependent protein kinase-1 [Homo sapiens] >gi_2505936_emb_CAA75341_(Y15056) PkB kinase [Homo sapiens] >gi_4505695_ref_NP_002604.1_pPDPK1_3-phosphoinositide dependent protein kinase-1

Seq. No. 6165
 Contig ID 6201_1.R1040
 5'-most EST rlr700899564.h1
 Method BLASTN
 NCBI GI g4519414
 BLAST score 182
 E value 1.0e-97
 Match length 470
 % identity 85
 NCBI Description Citrus unshiu (CitVATP c-2) mRNA for vacuolar H+-ATPase c subunit, complete cds

Seq. No. 6166
 Contig ID 6203_1.R1040
 5'-most EST LIB3029-006-Q1-B1-H1
 Method BLASTX
 NCBI GI g2829918
 BLAST score 194
 E value 8.0e-15
 Match length 71
 % identity 54
 NCBI Description (AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No. 6167
 Contig ID 6208_1.R1040
 5'-most EST kl1701203850.h1

Seq. No. 6168
 Contig ID 6217_1.R1040
 5'-most EST LIB3029-006-Q1-B1-E9

Seq. No. 6169
 Contig ID 6221_1.R1040
 5'-most EST hyd700726494.h1
 Method BLASTX
 NCBI GI g3212116
 BLAST score 277

Method BLASTN
 NCBI GI g436031
 BLAST score 112
 E value 9.0e-56
 Match length 328
 % identity 84
 NCBI Description Nicotiana tabacum (TSC40-4) 60S ribosomal protein L34 mRNA, complete cds

Seq. No. 6183
 Contig ID 6244_2.R1040
 5'-most EST LIB3039-035-Q1-E1-G6
 Method BLASTX
 NCBI GI g730558
 BLAST score 471
 E value 5.0e-47
 Match length 95
 % identity 95
 NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir_S48027 ribosomal protein L34 - common tobacco >gi_2129964_pir_S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi_436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi_436032 (L27107) 60S ribosomal protein L34 [Nicotiana tabacum]

Seq. No. 6184
 Contig ID 6244_3.R1040
 5'-most EST leu701149904.h1
 Method BLASTX
 NCBI GI g730557
 BLAST score 379
 E value 2.0e-36
 Match length 75
 % identity 95
 NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_2119150_pir_S60476 ribosomal protein L34 - garden pea >gi_498908 (U10047) ribosomal protein L34 homolog [Pisum sativum]

Seq. No. 6185
 Contig ID 6247_1.R1040
 5'-most EST jC-gmle01810005c06a1
 Method BLASTX
 NCBI GI g3183454
 BLAST score 648
 E value 2.0e-67
 Match length 278
 % identity 47
 NCBI Description HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION >gi_2632217_emb_CAA10859 (AJ222587) YkwC protein [Bacillus subtilis] >gi_2633767_emb_CAB13269 (Z99111) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]

Seq. No. 6186
 Contig ID 6247_2.R1040
 5'-most EST ncj700986168.h1
 Method BLASTX
 NCBI GI g3183454

Seq. No.	6192
Contig ID	6285_1.R1040
5'-most EST	LIB3029-005-Q1-B1-D10
Method	BLASTX
NCBI GI	g2244816
BLAST score	201
E value	1.0e-15
Match length	60
% identity	75
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.	6193
Contig ID	6290_1.R1040
5'-most EST	LIB3094-059-Q1-K1-C1
Method	BLASTX
NCBI GI	g729775
BLAST score	482
E value	1.0e-48
Match length	116
% identity	78
NCBI Description	HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR) >gi_100264_pir_S25481 heat shock transcription factor 8 - Peruvian tomato >gi_19492_emb_CAA47869_ (X67600) heat shock transcription factor 8 [Lycopersicon peruvianum]
Seq. No.	6194
Contig ID	6291_1.R1040
5'-most EST	LIB3049-023-Q1-E1-H9
Seq. No.	6195
Contig ID	6293_1.R1040
5'-most EST	kl1701205910.h1
Method	BLASTX
NCBI GI	g3915020
BLAST score	2619
E value	0.0e+00
Match length	639
% identity	85
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE) >gi_1022365_emb_CAA91217_ (Z56278) sucrose phosphate synthase [Vicia faba]
Seq. No.	6196
Contig ID	6295_1.R1040
5'-most EST	g4287190
Method	BLASTX
NCBI GI	g3434971
BLAST score	278
E value	2.0e-24
Match length	73
% identity	73
NCBI Description	(AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]
Seq. No.	6197

Contig ID 6295 2.R1040
 5'-most EST uxk700672508.h1
 Method BLASTX
 NCBI GI g1208496
 BLAST score 243
 E value 1.0e-20
 Match length 56
 % identity 82
 NCBI Description (D38124) EREBP-3 [Nicotiana tabacum]

Seq. No. 6198
 Contig ID 6301 1.R1040
 5'-most EST LIB3051-116-Q1-K1-G3
 Method BLASTX
 NCBI GI g3935184
 BLAST score 578
 E value 2.0e-59
 Match length 197
 % identity 56
 NCBI Description (AC004557) F17L21.27 [Arabidopsis thaliana]

Seq. No. 6199
 Contig ID 6307 1.R1040
 5'-most EST 6HA-02-Q1-B1-F1
 Method BLASTX
 NCBI GI g558606
 BLAST score 382
 E value 6.0e-37
 Match length 109
 % identity 62
 NCBI Description (X70688) Nthsp18p [Nicotiana tabacum]

Seq. No. 6200
 Contig ID 6313 1.R1040
 5'-most EST pmv700892451.h1
 Method BLASTN
 NCBI GI g2997590
 BLAST score 523
 E value 0.0e+00
 Match length 1032
 % identity 88
 NCBI Description Pisum sativum glucose-6-phosphate/phosphate-translocator precursor (GPT) mRNA, nuclear gene encoding plastid protein, complete cds

Seq. No. 6201
 Contig ID 6313 2.R1040
 5'-most EST jex700908125.h1
 Method BLASTN
 NCBI GI g2997590
 BLAST score 156
 E value 2.0e-82
 Match length 329
 % identity 91
 NCBI Description Pisum sativum glucose-6-phosphate/phosphate-translocator precursor (GPT) mRNA, nuclear gene encoding plastid protein, complete cds

NCBI Description (AF014955) TFAR19 [Homo sapiens]

Seq. No. 6209
Contig ID 6326_1.R1040
5'-most EST LIB3029-004-Q1-B1-F11

Seq. No. 6210
Contig ID 6331_1.R1040
5'-most EST LIB3072-060-Q1-K1-D7
Method BLASTN
NCBI GI g18653
BLAST score 508
E value 0.0e+00
Match length 548
% identity 98
NCBI Description Soybean gene for heat shock protein Gmhsp18.5-C (class I)

Seq. No. 6211
Contig ID 6331_2.R1040
5'-most EST g5606297
Method BLASTN
NCBI GI g18653
BLAST score 290
E value 1.0e-162
Match length 579
% identity 89
NCBI Description Soybean gene for heat shock protein Gmhsp18.5-C (class I)

Seq. No. 6212
Contig ID 6331_3.R1040
5'-most EST LIB3170-041-Q1-J1-A9
Method BLASTN
NCBI GI g18655
BLAST score 631
E value 0.0e+00
Match length 813
% identity 95
NCBI Description Soybean heat-shock gene hs6871 sequence

Seq. No. 6213
Contig ID 6331_4.R1040
5'-most EST epX701105644.h1
Method BLASTN
NCBI GI g18655
BLAST score 251
E value 1.0e-139
Match length 387
% identity 93
NCBI Description Soybean heat-shock gene hs6871 sequence

Seq. No. 6214
Contig ID 6331_5.R1040
5'-most EST epX701107217.h1
Method BLASTN
NCBI GI g18655
BLAST score 396
E value 0.0e+00

09684016 " 101000

Seq. No. 6226
Contig ID 6348_1.R1040
5'-most EST LIB3029-004-Q1-B1-E5
Method BLASTX
NCBI GI g2213590
BLAST score 216
E value 3.0e-17
Match length 128
% identity 38
NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No. 6227
Contig ID 6350_1.R1040
5'-most EST LIB3072-024-Q1-E1-G1
Method BLASTN
NCBI GI g460802
BLAST score 54
E value 3.0e-21
Match length 238
% identity 81
NCBI Description P.amygdalus, Batsch (Texas) ole1 mRNA

Seq. No. 6228
Contig ID 6350_2.R1040
5'-most EST LIB3072-056-Q1-K1-D10
Method BLASTX
NCBI GI g3914199
BLAST score 222
E value 5.0e-18
Match length 141
% identity 40
NCBI Description OLEOSIN 1 >gi_460803_emb_CAA55008_ (X78118) oleosin [Prunus dulcis]

Seq. No. 6229
Contig ID 6354_1.R1040
5'-most EST g5606027
Method BLASTX
NCBI GI g3688188
BLAST score 2538
E value 0.0e+00
Match length 608
% identity 80
NCBI Description (AL031804) pyruvate decarboxylase-1 (Pdc1) [Arabidopsis thaliana]

Seq. No. 6230
Contig ID 6354_3.R1040
5'-most EST txt700734851.h1
Method BLASTN
NCBI GI g1177604
BLAST score 165
E value 1.0e-87
Match length 429
% identity 88
NCBI Description P.sativum mRNA for pyruvate decarboxylase (PDC2)

Seq. No. 6231
 Contig ID 6354_4.R1040
 5'-most EST bnu700967544.h1
 Method BLASTX
 NCBI GI g3688188
 BLAST score 306
 E value 6.0e-28
 Match length 94
 % identity 66
 NCBI Description (AL031804) pyruvate decarboxylase-1 (Pdc1) [Arabidopsis thaliana]

Seq. No. 6232
 Contig ID 6359_1.R1040
 5'-most EST uC-gmflminsoy055c05b1
 Method BLASTX
 NCBI GI g4006829
 BLAST score 707
 E value 2.0e-74
 Match length 207
 % identity 67
 NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No. 6233
 Contig ID 6359_2.R1040
 5'-most EST kl1701211035.h1
 Method BLASTX
 NCBI GI g3805765
 BLAST score 161
 E value 8.0e-11
 Match length 48
 % identity 67
 NCBI Description (AC005693) putative protein kinase [Arabidopsis thaliana]

Seq. No. 6234
 Contig ID 6359_3.R1040
 5'-most EST ssr700553651.h1

Seq. No. 6235
 Contig ID 6361_1.R1040
 5'-most EST uaw700663807.h1
 Method BLASTX
 NCBI GI g452519
 BLAST score 181
 E value 1.0e-12
 Match length 131
 % identity 20
 NCBI Description (D26362) similar to Human homolog of Drosophila female sterile homeotic mRNA (HUMFSHG) [Homo sapiens]

Seq. No. 6236
 Contig ID 6362_1.R1040
 5'-most EST txt700731402.h1
 Method BLASTN
 NCBI GI g18638
 BLAST score 318

Seq. No. 6242
 Contig ID 6386_1.R1040
 5'-most EST zpv700758409.h1
 Method BLASTX
 NCBI GI g633890
 BLAST score 973
 E value 1.0e-105
 Match length 280
 % identity 69
 NCBI Description (S72926) glucose and ribitol dehydrogenase homolog [Hordeum vulgare]

Seq. No. 6243
 Contig ID 6386_4.R1040
 5'-most EST uxk700668322.h1
 Method BLASTX
 NCBI GI g633890
 BLAST score 170
 E value 5.0e-12
 Match length 44
 % identity 73
 NCBI Description (S72926) glucose and ribitol dehydrogenase homolog [Hordeum vulgare]

Seq. No. 6244
 Contig ID 6390_1.R1040
 5'-most EST LIB3039-010-Q1-E1-C8
 Method BLASTX
 NCBI GI g3617770
 BLAST score 552
 E value 1.0e-56
 Match length 138
 % identity 73
 NCBI Description (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 6245
 Contig ID 6390_2.R1040
 5'-most EST LIB3029-003-Q1-B1-G10
 Method BLASTX
 NCBI GI g2501064
 BLAST score 302
 E value 2.0e-27
 Match length 113
 % identity 58
 NCBI Description PROBABLE THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (THREONINE--TRNA LIGASE) (THRRS) >gi_2191162 (AF007270) Similar to threonyl-tRNA synthetase; coded for by A. thaliana cDNA R65376 [Arabidopsis thaliana]

Seq. No. 6246
 Contig ID 6397_1.R1040
 5'-most EST LIB3072-011-Q1-E1-D1
 Method BLASTN
 NCBI GI g1141781
 BLAST score 233
 E value 1.0e-128
 Match length 317


```

% identity      93
NCBI Description Vigna radiata EM protein mRNA, complete cds

Seq. No.        6247
Contig ID       6399_1.R1040
5'-most EST     txt700734368.h1

Seq. No.        6248
Contig ID       6399_2.R1040
5'-most EST     crh700853112.h1

Seq. No.        6249
Contig ID       6400_1.R1040
5'-most EST     LIB3029-003-Q1-B1-E11
Method          BLASTX
NCBI GI         g3738230
BLAST score     286
E value         1.0e-25
Match length    85
% identity      60
NCBI Description (AB007790) DREB2A [Arabidopsis thaliana]
>gi_4126706_dbj_BAA36705_ (AB016570) DREB2A [Arabidopsis
thaliana]

Seq. No.        6250
Contig ID       6401_1.R1040
5'-most EST     uC-gmrominsoy047c11b1
Method          BLASTX
NCBI GI         g1001449
BLAST score     154
E value         6.0e-10
Match length    91
% identity      41
NCBI Description (D63999) hypothetical protein [Synechocystis sp.]

Seq. No.        6251
Contig ID       6404_1.R1040
5'-most EST     LIB3139-022-P1-N1-H3
Method          BLASTX
NCBI GI         g3551958
BLAST score     714
E value         2.0e-75
Match length    197
% identity      68
NCBI Description (AF082032) senescence-associated protein 12 [Hemerocallis
hybrid cultivar]

Seq. No.        6252
Contig ID       6404_2.R1040
5'-most EST     uC-gmrominsoy207h01b1
Method          BLASTX
NCBI GI         g2708750
BLAST score     501
E value         2.0e-50
Match length    253
% identity      46
NCBI Description (AC003952) putative physical impedance protein [Arabidopsis

```


Match length 193
 % identity 47
 NCBI Description RNA-binding protein RZ-1 - wood tobacco
 >gi_1395193_dbj_BAA12064_ (D83696) RNA-binding protein RZ-1
 [Nicotiana sylvestris] >gi_1435062_dbj_BAA06012_ (D28861)
 RNA binding protein, RZ-1 [Nicotiana sylvestris]

Seq. No. 6264
 Contig ID 6416_1.R1040
 5'-most EST LIB3029-003-Q1-B1-C4

Seq. No. 6265
 Contig ID 6428_1.R1040
 5'-most EST uC-gmflminsoy056c09b1
 Method BLASTX
 NCBI GI g4049341
 BLAST score 166
 E value 3.0e-11
 Match length 146
 % identity 35
 NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 6266
 Contig ID 6433_1.R1040
 5'-most EST ncj700987169.h1
 Method BLASTX
 NCBI GI g169363
 BLAST score 377
 E value 9.0e-36
 Match length 151
 % identity 54
 NCBI Description (M75856) PVPR3 [Phaseolus vulgaris]

Seq. No. 6267
 Contig ID 6433_2.R1040
 5'-most EST LIB3087-001-Q1-K1-D6

Seq. No. 6268
 Contig ID 6434_1.R1040
 5'-most EST LIB3107-021-Q1-K1-E3

Seq. No. 6269
 Contig ID 6434_2.R1040
 5'-most EST LIB3051-002-Q1-E1-H11

Seq. No. 6270
 Contig ID 6435_1.R1040
 5'-most EST gsv701054428.h1

Seq. No. 6271
 Contig ID 6440_1.R1040
 5'-most EST LIB3074-035-Q1-K1-C9
 Method BLASTX
 NCBI GI g3377820
 BLAST score 436
 E value 5.0e-43
 Match length 123

% identity 70
 NCBI Description (AF076275) contains similarity to coatomer zeta chains
 [Arabidopsis thaliana]

Seq. No. 6272
 Contig ID 6440_2.R1040
 5'-most EST LIB3040-023-Q1-E1-D9
 Method BLASTX
 NCBI GI g3377820
 BLAST score 280
 E value 5.0e-25
 Match length 64
 % identity 80
 NCBI Description (AF076275) contains similarity to coatomer zeta chains
 [Arabidopsis thaliana]

Seq. No. 6273
 Contig ID 6441_1.R1040
 5'-most EST g4292967
 Method BLASTN
 NCBI GI g438898
 BLAST score 136
 E value 3.0e-70
 Match length 407
 % identity 85
 NCBI Description Soybean glutamine phosphoribosylpyrophosphate
 amidotransferase mRNA, complete cds

Seq. No. 6274
 Contig ID 6442_1.R1040
 5'-most EST trc700561456.h1

Seq. No. 6275
 Contig ID 6442_2.R1040
 5'-most EST LIB3072-015-Q1-E1-D10

Seq. No. 6276
 Contig ID 6445_1.R1040
 5'-most EST gsv701046109.h1

Seq. No. 6277
 Contig ID 6445_2.R1040
 5'-most EST uC-gmropic038e03b1

Seq. No. 6278
 Contig ID 6452_1.R1040
 5'-most EST uaw700666570.h1
 Method BLASTN
 NCBI GI g534940
 BLAST score 57
 E value 4.0e-23
 Match length 78
 % identity 93
 NCBI Description S.tuberosum mitochondrial DNA for ribosomal protein S10

Seq. No. 6279
 Contig ID 6453_1.R1040

09684015-101000

BLAST score 398
 E value 1.0e-38
 Match length 123
 % identity 65
 NCBI Description RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_
 (D26182) RNA-binding glycine rich protein (RGP-2)
 [Nicotiana sylvestris]

Seq. No. 6293
 Contig ID 6478_2.R1040
 5'-most EST jC-gmst02400028g05a1
 Method BLASTX
 NCBI GI g2493318
 BLAST score 453
 E value 6.0e-45
 Match length 102
 % identity 83
 NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_
 (Z25471) blue copper protein [Pisum sativum]
 >gi_1098264_prf_2115352A blue Cu protein [Pisum sativum]

Seq. No. 6294
 Contig ID 6478_3.R1040
 5'-most EST uC-gmrominsoy316g06b1
 Method BLASTX
 NCBI GI g1084415
 BLAST score 344
 E value 2.0e-32
 Match length 110
 % identity 65
 NCBI Description RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_
 (D26182) RNA-binding glycine rich protein (RGP-2)
 [Nicotiana sylvestris]

Seq. No. 6295
 Contig ID 6478_4.R1040
 5'-most EST LIB3094-002-Q1-K1-G1
 Method BLASTX
 NCBI GI g1084415
 BLAST score 307
 E value 4.0e-28
 Match length 107
 % identity 59
 NCBI Description RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_
 (D26182) RNA-binding glycine rich protein (RGP-2)
 [Nicotiana sylvestris]

Seq. No. 6296
 Contig ID 6488_1.R1040
 5'-most EST kmv700740304.h1
 Method BLASTX
 NCBI GI g2500426
 BLAST score 343
 E value 9.0e-32
 Match length 124
 % identity 56
 NCBI Description 30S RIBOSOMAL PROTEIN S9 >gi_1652399_dbj_BAA17321_ (D90905)

30S ribosomal protein S9 [Synechocystis sp.]

Seq. No. 6297
 Contig ID 6489_1.R1040
 5'-most EST rca700997926.h1
 Method BLASTX
 NCBI GI g1931652
 BLAST score 209
 E value 2.0e-16
 Match length 101
 % identity 50
 NCBI Description (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog [Arabidopsis thaliana]

Seq. No. 6298
 Contig ID 6498_1.R1040
 5'-most EST LIB3029-001-Q1-B1-H10

Seq. No. 6299
 Contig ID 6500_1.R1040
 5'-most EST uC-gmronoir008d08b1
 Method BLASTX
 NCBI GI g3738320
 BLAST score 459
 E value 3.0e-45
 Match length 303
 % identity 36
 NCBI Description (AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No. 6300
 Contig ID 6500_2.R1040
 5'-most EST LIB3051-010-Q1-E1-D4
 Method BLASTX
 NCBI GI g3738320
 BLAST score 280
 E value 7.0e-25
 Match length 129
 % identity 40
 NCBI Description (AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No. 6301
 Contig ID 6520_1.R1040
 5'-most EST hyd700728002.h1
 Method BLASTX
 NCBI GI g2880051
 BLAST score 227
 E value 4.0e-18
 Match length 101
 % identity 47
 NCBI Description (AC002340) putative protein kinase [Arabidopsis thaliana]

Seq. No. 6302
 Contig ID 6522_1.R1040
 5'-most EST dpv701097360.h1
 Method BLASTX

NCBI GI g4165018
 BLAST score 1037
 E value 1.0e-156
 Match length 615
 % identity 48
 NCBI Description (D89053) Acyl-CoA synthetase 3 [Homo sapiens]

Seq. No. 6303
 Contig ID 6522_2.R1040
 5'-most EST LIB3029-001-Q1-B1-D4
 Method BLASTX
 NCBI GI g1468969
 BLAST score 172
 E value 6.0e-12
 Match length 56
 % identity 55
 NCBI Description (D30666) brain acyl-CoA synthtase II [Rattus norvegicus]

Seq. No. 6304
 Contig ID 6522_3.R1040
 5'-most EST uaw700662748.h1
 Method BLASTX
 NCBI GI g1468969
 BLAST score 380
 E value 1.0e-36
 Match length 134
 % identity 57
 NCBI Description (D30666) brain acyl-CoA synthtase II [Rattus norvegicus]

Seq. No. 6305
 Contig ID 6526_1.R1040
 5'-most EST kl1701206060.h1
 Method BLASTX
 NCBI GI g3482913
 BLAST score 646
 E value 2.0e-67
 Match length 253
 % identity 52
 NCBI Description (AC003970) Similar to MtN21, gi_2598575, Megicago truncatula nodulation induced gene [Arabidopsis thaliana]

Seq. No. 6306
 Contig ID 6532_1.R1040
 5'-most EST LIB3040-015-Q1-E1-C6

Seq. No. 6307
 Contig ID 6532_2.R1040
 5'-most EST LIB3040-053-Q1-E1-F12

Seq. No. 6308
 Contig ID 6533_1.R1040
 5'-most EST crh700851849.h1
 Method BLASTX
 NCBI GI g265975
 BLAST score 173
 E value 8.0e-12
 Match length 134

BLAST score 341
E value 4.0e-32
Match length 120
% identity 58
NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No. 6316
Contig ID 6545_1.R1040
5'-most EST gsv701051793.h1
Method BLASTX
NCBI GI g132659
BLAST score 732
E value 2.0e-77
Match length 241
% identity 60
NCBI Description 50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13)
>gi_81483_pir__A32033 ribosomal protein L13 precursor,
chloroplast - spinach >gi_170133 (J04461) ribosomal protein
L13 [Spinacia oleracea]

Seq. No. 6317
Contig ID 6551_1.R1040
5'-most EST uC-gmronoir007f09b1
Method BLASTX
NCBI GI g2911058
BLAST score 275
E value 2.0e-38
Match length 112
% identity 71
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 6318
Contig ID 6551_2.R1040
5'-most EST jC-gmst02400002c05a1

Seq. No. 6319
Contig ID 6560_1.R1040
5'-most EST fC-gmse7000763420f1
Method BLASTX
NCBI GI g3413699
BLAST score 473
E value 3.0e-47
Match length 115
% identity 73
NCBI Description (AC004747) putative heat shock protein [Arabidopsis thaliana]

Seq. No. 6320
Contig ID 6596_1.R1040
5'-most EST LIB3029-009-Q1-B1-F4

Seq. No. 6321
Contig ID 6598_1.R1040
5'-most EST LIB3170-086-Q1-J1-C3
Method BLASTN
NCBI GI g2924257

0000000000000000000000000000000000

```
Seq. No.          6333
Contig ID         6638_1.R1040
5'-most EST      jC-gm1e01810021b02a1
Method            BLASTX
NCBI GI           g3080407
BLAST score       424
E value           1.0e-84
Match length      221
% identity        73
NCBI Description  (AL022604) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.          6335
Contig ID         6639_1.R1040
5'-most EST      gsv701049521.h1
Method           BLASTX
NCBI GI          g461736
BLAST score      1763
E value          0.0e+00
Match length     385
% identity       91
NCBI Description  MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR
                  >gi_478786_pir_S29316 chaperonin 60 - cucurbit
                  >gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita
                  sp.]
```

Seq. No.	6337
Contig ID	6643_2.R1040
5'-most EST	jC-qmst02400029a10a1

Seq. No.	6350
Contig ID	6672_1.R1040
5'-most EST	LIB3030-012-Q1-B1-B10
Seq. No.	6351
Contig ID	6673_1.R1040
5'-most EST	uC-gmflminsoy024d02b1
Seq. No.	6352
Contig ID	6678_1.R1040
5'-most EST	sat701014952.h1
Seq. No.	6353
Contig ID	6683_1.R1040
5'-most EST	rlr700900487.h1
Method	BLASTX
NCBI GI	g2708532
BLAST score	970
E value	1.0e-105
Match length	301
% identity	32
NCBI Description	(AF029351) putative RNA binding protein [Nicotiana tabacum]
Seq. No.	6354
Contig ID	6687_1.R1040
5'-most EST	jC-gmle01810000g09a1
Seq. No.	6355
Contig ID	6687_2.R1040
5'-most EST	zpv700760473.h1
Seq. No.	6356
Contig ID	6694_1.R1040
5'-most EST	LIB3030-011-Q1-B1-H10
Method	BLASTX
NCBI GI	g1504020
BLAST score	122
E value	6.0e-10
Match length	55
% identity	67
NCBI Description	(D86973) similar to Yeast translation activator GCN1 (P1:A48126) [Homo sapiens]
Seq. No.	6357
Contig ID	6699_1.R1040
5'-most EST	LIB3051-103-Q1-K1-G7
Method	BLASTX
NCBI GI	g461812
BLAST score	414
E value	2.0e-40
Match length	193
% identity	44
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus

roseus]

Seq. No. 6358
Contig ID 6699_2.R1040
5'-most EST uC-gmronoir043h10b1

Seq. No. 6359
Contig ID 6699_5.R1040
5'-most EST zhf700952542.h1

Seq. No. 6360
Contig ID 6699_6.R1040
5'-most EST zhf700961126.h1

Seq. No. 6361
Contig ID 6703_1.R1040
5'-most EST LIB3030-012-Q1-B1-A12
Method BLASTX
NCBI GI g4467124
BLAST score 172
E value 3.0e-12
Match length 107
% identity 43
NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6362
Contig ID 6703_2.R1040
5'-most EST jC-gmf102220102h03a1
Method BLASTX
NCBI GI g4467124
BLAST score 159
E value 1.0e-10
Match length 43
% identity 70
NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6363
Contig ID 6704_1.R1040
5'-most EST LIB3030-011-Q1-B1-B11
Method BLASTX
NCBI GI g4006915
BLAST score 215
E value 3.0e-17
Match length 111
% identity 44
NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6364
Contig ID 6706_1.R1040
5'-most EST zhf700965022.h1
Method BLASTX
NCBI GI g4415908
BLAST score 431
E value 3.0e-42
Match length 152
% identity 49
NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

E value 2.0e-32
 Match length 96
 % identity 79
 NCBI Description (AF067961) homeodomain protein [Malus domestica]

Seq. No. 6407
 Contig ID 6774_1.R1040
 5'-most EST gsv701056309.h1

Seq. No. 6408
 Contig ID 6774_2.R1040
 5'-most EST hrw701060177.h1

Seq. No. 6409
 Contig ID 6775_1.R1040
 5'-most EST fde700876739.h1
 Method BLASTX
 NCBI GI g4522012
 BLAST score 899
 E value 7.0e-97
 Match length 310
 % identity 57
 NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6410
 Contig ID 6778_1.R1040
 5'-most EST pxt700946334.h1
 Method BLASTX
 NCBI GI g3063470
 BLAST score 396
 E value 2.0e-38
 Match length 70
 % identity 97
 NCBI Description (AC003981) F22013.32 [Arabidopsis thaliana]

Seq. No. 6411
 Contig ID 6782_1.R1040
 5'-most EST uC-gmrominsoy243g03b1

Seq. No. 6412
 Contig ID 6782_2.R1040
 5'-most EST awf700840314.h1

Seq. No. 6413
 Contig ID 6782_3.R1040
 5'-most EST uC-gmflminsoy078f04b1

Seq. No. 6414
 Contig ID 6783_1.R1040
 5'-most EST uC-gmrominsoy142c04b1
 Method BLASTX
 NCBI GI g3540219
 BLAST score 891
 E value 5.0e-96
 Match length 390
 % identity 46
 NCBI Description (D87686) KIAA0017 protein [Homo sapiens]

Seq. No. 6415
 Contig ID 6784_1.R1040
 5'-most EST uaw700661165.h1
 Method BLASTX
 NCBI GI g322787
 BLAST score 755
 E value 7.0e-80
 Match length 348
 % identity 46
 NCBI Description pyruvate kinase (EC 2.7.1.40), cytosolic - potato

Seq. No. 6416
 Contig ID 6784_2.R1040
 5'-most EST jC-gmst02400072a04a1

Seq. No. 6417
 Contig ID 6785_1.R1040
 5'-most EST LIB3030-010-Q1-B1-B3

Seq. No. 6418
 Contig ID 6787_1.R1040
 5'-most EST LIB3030-009-Q1-B1-G5
 Method BLASTX
 NCBI GI g3292830
 BLAST score 346
 E value 4.0e-32
 Match length 263
 % identity 37
 NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 6419
 Contig ID 6791_1.R1040
 5'-most EST uC-gmflminsoy018e10b1
 Method BLASTX
 NCBI GI g2828151
 BLAST score 302
 E value 2.0e-27
 Match length 100
 % identity 59
 NCBI Description (AF042386) cyclophilin-33B [Homo sapiens]
 >gi_4406229_gb_AAD19907_ (AF104013) peptidyl-prolyl
 cis-trans isomerase E [Homo sapiens]

Seq. No. 6420
 Contig ID 6796_1.R1040
 5'-most EST LIB3030-009-Q1-B1-H7
 Method BLASTX
 NCBI GI g4263704
 BLAST score 526
 E value 3.0e-53
 Match length 239
 % identity 43
 NCBI Description (AC006223) putative sugar starvation-induced protein
 [Arabidopsis thaliana]

Seq. No. 6421

NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6426
Contig ID 6804_3.R1040
5'-most EST zpv700763346.h1
Method BLASTX
NCBI GI g1922242
BLAST score 210
E value 1.0e-16
Match length 53
% identity 85

NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6427
Contig ID 6805_1.R1040
5'-most EST LIB3030-009-Q1-B1-G1
Method BLASTX
NCBI GI g2462828
BLAST score 298
E value 5.0e-27
Match length 118
% identity 46

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6428
Contig ID 6805_2.R1040
5'-most EST zsg701124373.h1
Method BLASTX
NCBI GI g2462828
BLAST score 167
E value 6.0e-12
Match length 59
% identity 47

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6429
Contig ID 6806_1.R1040
5'-most EST jC-gmro02910014f01a1
Method BLASTX
NCBI GI g4508083
BLAST score 500
E value 3.0e-50
Match length 307
% identity 7

NCBI Description (AC005882) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 6430
Contig ID 6807_1.R1040
5'-most EST LIB3170-007-Q1-K1-D10
Method BLASTX
NCBI GI g3687251
BLAST score 542
E value 3.0e-55
Match length 142
% identity 73

NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

Seq. No.	6431
Contig ID	6810_1.R1040
5'-most EST	LIB3049-001-Q1-E1-G8
Method	BLASTX
NCBI GI	g2213625
BLAST score	478
E value	1.0e-47
Match length	169
% identity	54
NCBI Description	(AC000103) F21J9.17 [Arabidopsis thaliana]
Seq. No.	6432
Contig ID	6810_2.R1040
5'-most EST	LIB3030-009-Q1-B1-D9
Seq. No.	6433
Contig ID	6810_4.R1040
5'-most EST	pxt700941967.h1
Seq. No.	6434
Contig ID	6811_1.R1040
5'-most EST	uC-gmflminsoy008h02b1
Method	BLASTX
NCBI GI	g232024
BLAST score	234
E value	6.0e-19
Match length	253
% identity	34
NCBI Description	PROTEIN E6 >gi_421806_pir_A46130 fiber protein - upland cotton >gi_2129498_pir_S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]
Seq. No.	6435
Contig ID	6811_2.R1040
5'-most EST	g4295094
Method	BLASTX
NCBI GI	g167324
BLAST score	170
E value	1.0e-11
Match length	191
% identity	46
NCBI Description	(M92051) 5' start site is putative; putative [Gossypium hirsutum]
Seq. No.	6436
Contig ID	6812_1.R1040
5'-most EST	LIB3065-008-Q1-N1-F6
Method	BLASTX
NCBI GI	g2245080
BLAST score	151
E value	9.0e-10
Match length	80
% identity	45
NCBI Description	(Z97343) myosin heavy chain homolog [Arabidopsis thaliana]

Contig ID	6830_1.R1040
5'-most EST	pxt700945726.h1
Method	BLASTN
NCBI GI	g1223921
BLAST score	127
E value	5.0e-65
Match length	331
% identity	85
NCBI Description	Vigna radiata vicilin peptidohydrolase, cysteinyl endopeptidase mRNA, complete cds
Seq. No.	6445
Contig ID	6832_1.R1040
5'-most EST	jC-gmle01810024f07a1
Seq. No.	6446
Contig ID	6832_2.R1040
5'-most EST	LIB3030-009-Q1-B1-B7
Seq. No.	6447
Contig ID	6832_3.R1040
5'-most EST	LIB3138-120-Q1-N1-E4
Seq. No.	6448
Contig ID	6835_1.R1040
5'-most EST	LIB3030-009-Q1-B1-A6
Method	BLASTX
NCBI GI	g632149
BLAST score	366
E value	2.0e-34
Match length	256
% identity	38
NCBI Description	narbonin - Vicia pannonica >gi_396829_emb_CAA80981_ (Z25534) narbonin [Vicia pannonica]
Seq. No.	6449
Contig ID	6836_1.R1040
5'-most EST	zhf700965238.h1
Method	BLASTX
NCBI GI	g1362162
BLAST score	184
E value	7.0e-39
Match length	173
% identity	53
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.	6450
Contig ID	6841_2.R1040
5'-most EST	LIB3139-068-P1-N1-H10
Seq. No.	6451
Contig ID	6844_1.R1040
5'-most EST	LIB3170-053-Q1-K1-A5
Method	BLASTX
NCBI GI	g1330401
BLAST score	206

E value 5.0e-16
 Match length 118
 % identity 36
 NCBI Description (U58762) T27F7.1 gene product [Caenorhabditis elegans]

Seq. No. 6452
 Contig ID 6844_3.R1040
 5'-most EST LIB3030-008-Q1-B1-H9

Seq. No. 6453
 Contig ID 6845_1.R1040
 5'-most EST LIB3092-010-Q1-K1-E11

Seq. No. 6454
 Contig ID 6846_1.R1040
 5'-most EST LIB3107-014-Q1-K1-G8
 Method BLASTX
 NCBI GI g2132930
 BLAST score 395
 E value 4.0e-38
 Match length 155
 % identity 49
 NCBI Description probable membrane protein YOR262w - yeast (Saccharomyces cerevisiae) >gi_1420591_emb_CAA99484_ (Z75170) ORF YOR262w [Saccharomyces cerevisiae]

Seq. No. 6455
 Contig ID 6847_1.R1040
 5'-most EST LIB3030-008-Q1-B1-H10
 Method BLASTX
 NCBI GI g2244792
 BLAST score 172
 E value 8.0e-12
 Match length 151
 % identity 34
 NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No. 6456
 Contig ID 6848_1.R1040
 5'-most EST LIB3030-008-Q1-B1-F4
 Method BLASTX
 NCBI GI g1483218
 BLAST score 369
 E value 3.0e-35
 Match length 164
 % identity 50
 NCBI Description (X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No. 6457
 Contig ID 6850_1.R1040
 5'-most EST k11701203944.h2
 Method BLASTX
 NCBI GI g3193301
 BLAST score 677
 E value 6.0e-71
 Match length 247

% identity 51
NCBI Description (AF069298) Arabidopsis putative chloroplast outer envelope
86-like protein T10P11.19 (GB: AC002330) [Arabidopsis
thaliana]

Seq. No. 6458
Contig ID 6851_1.R1040
5'-most EST ssr700554846.h1

Seq. No. 6459
Contig ID 6856_1.R1040
5'-most EST leu701156170.h1
Method BLASTX
NCBI GI g1107526
BLAST score 1116
E value 1.0e-122
Match length 351
% identity 63
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 6460
Contig ID 6856_2.R1040
5'-most EST g5753379
Method BLASTX
NCBI GI g2983289
BLAST score 154
E value 5.0e-10
Match length 73
% identity 42
NCBI Description (AE000703) chaperone DnaJ [Aquifex aeolicus]

Seq. No. 6461
Contig ID 6858_1.R1040
5'-most EST epx701104218.h1
Method BLASTX
NCBI GI g3702339
BLAST score 1046
E value 1.0e-114
Match length 340
% identity 61
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 6462
Contig ID 6861_1.R1040
5'-most EST LIB3051-049-Q1-K1-B3
Method BLASTX
NCBI GI g4164473
BLAST score 367
E value 1.0e-34
Match length 105
% identity 69
NCBI Description (AF061157) negatively light-regulated protein [Vernicia
fordii]

Seq. No. 6463
Contig ID 6861_2.R1040
5'-most EST sat701002758.h2

NCBI GI	g3702314
BLAST score	426
E value	6.0e-42
Match length	135
% identity	60
NCBI Description	(AC002535) similar to SWI/SNF complex subunit BAF170 [Arabidopsis thaliana]
Seq. No.	6469
Contig ID	6866_1.R1040
5'-most EST	LIB3030-008-Q1-B1-E11
Method	BLASTX
NCBI GI	g3047116
BLAST score	163
E value	3.0e-11
Match length	38
% identity	89
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	6470
Contig ID	6868_1.R1040
5'-most EST	uC-gmrominsoy126d11b1
Seq. No.	6471
Contig ID	6869_1.R1040
5'-most EST	vwf700676052.h1
Method	BLASTX
NCBI GI	g4191616
BLAST score	635
E value	3.0e-66
Match length	234
% identity	53
NCBI Description	(AF120334) GTP-binding protein NGB [Homo sapiens]
Seq. No.	6472
Contig ID	6871_1.R1040
5'-most EST	jC-gmfl02220132ab02d1
Seq. No.	6473
Contig ID	6872_1.R1040
5'-most EST	fde700876618.h1
Method	BLASTX
NCBI GI	g2213584
BLAST score	827
E value	3.0e-88
Match length	295
% identity	55
NCBI Description	(AC000348) T7N9.4 [Arabidopsis thaliana]
Seq. No.	6474
Contig ID	6874_1.R1040
5'-most EST	kl1701208032.h1
Method	BLASTX
NCBI GI	g2330647
BLAST score	688
E value	4.0e-72
Match length	288

Match length 147
 % identity 65
 NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 6482
 Contig ID 6878_3.R1040
 5'-most EST kl1701206730.h1
 Method BLASTX
 NCBI GI g1619602
 BLAST score 272
 E value 2.0e-24
 Match length 63
 % identity 81
 NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 6483
 Contig ID 6880_1.R1040
 5'-most EST LIB3051-022-Q1-K1-D4
 Method BLASTX
 NCBI GI g1708975
 BLAST score 448
 E value 7.0e-44
 Match length 396
 % identity 35
 NCBI Description METHIONINE GAMMA-LYASE (L-METHIONINASE)
 >gi_1084040_pir_JC4174-methionine gamma-lyase (EC
 4.4.1.11) - Pseudomonas putida >gi_902932_dbj_BAA13642_
 (D88554) L-methionine gamma-lyase [Pseudomonas putida]
 >gi_2217945_dbj_BAA20553_ (D89015) L-methionine gamma-lyase
 [Pseudomonas putida] >gi_1096717_prf_2112270A Met
 gamma-lyase [Pseudomonas putida]

Seq. No. 6484
 Contig ID 6880_2.R1040
 5'-most EST g5606623
 Method BLASTX
 NCBI GI g1709007
 BLAST score 172
 E value 4.0e-12
 Match length 102
 % identity 38
 NCBI Description O-SUCCINYLMOMOSERINE SULFHYDRYLASE (OSH SULFHYDRYLASE)
 >gi_607830 (U10904) O-succinylhomoserine sulfhydrylase
 [Pseudomonas aeruginosa]

Seq. No. 6485
 Contig ID 6880_3.R1040
 5'-most EST LIB3065-005-Q1-N1-A2

Seq. No. 6486
 Contig ID 6881_1.R1040
 5'-most EST LIB3056-004-Q1-N1-D10
 Method BLASTX
 NCBI GI g481815
 BLAST score 195
 E value 1.0e-14
 Match length 188

NCBI GI g2052508
 BLAST score 917
 E value 1.0e-120
 Match length 360
 % identity 61
 NCBI Description (U95759) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]

Seq. No. 6493
 Contig ID 6891_2.R1040
 5'-most EST zhf700963155.h1
 Method BLASTX
 NCBI GI g2052510
 BLAST score 858
 E value 2.0e-92
 Match length 232
 % identity 72
 NCBI Description (U95758) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]

Seq. No. 6494
 Contig ID 6894_1.R1040
 5'-most EST vwf700674245.h1

Seq. No. 6495
 Contig ID 6894_2.R1040
 5'-most EST fde700873040.h1

Seq. No. 6496
 Contig ID 6897_1.R1040
 5'-most EST jex700905170.h1
 Method BLASTX
 NCBI GI g2979553
 BLAST score 586
 E value 3.0e-60
 Match length 291
 % identity 40
 NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6497
 Contig ID 6899_1.R1040
 5'-most EST uC-gmflminsoy008e10b1
 Method BLASTX
 NCBI GI g416758
 BLAST score 338
 E value 3.0e-35
 Match length 124
 % identity 59
 NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana]
 >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No. 6498
 Contig ID 6901_1.R1040
 5'-most EST zhf700952535.h1
 Method BLASTN

5'-most EST LIB3051-067-Q1-K1-A11
 Method BLASTX
 NCBI GI g2982266
 BLAST score 452
 E value 5.0e-45
 Match length 104
 % identity 82
 NCBI Description (AF051216) probable fibrillarin [Picea mariana]

Seq. No. 6510
 Contig ID 6925_5.R1040
 5'-most EST vzy700754605.h1
 Method BLASTX
 NCBI GI g2982266
 BLAST score 433
 E value 1.0e-42
 Match length 97
 % identity 82
 NCBI Description (AF051216) probable fibrillarin [Picea mariana]

Seq. No. 6511
 Contig ID 6925_6.R1040
 5'-most EST jC-gmst02400009b07a1

Seq. No. 6512
 Contig ID 6925_7.R1040
 5'-most EST jsh701067142.h1
 Method BLASTN
 NCBI GI g21002
 BLAST score 84
 E value 1.0e-39
 Match length 206
 % identity 9
 NCBI Description Bean DNA for glycine-rich cell wall protein GRP 1.8

Seq. No. 6513
 Contig ID 6926_1.R1040
 5'-most EST rlr700897678.h1

Seq. No. 6514
 Contig ID 6933_1.R1040
 5'-most EST g4305391
 Method BLASTX
 NCBI GI g2576411
 BLAST score 745
 E value 5.0e-85
 Match length 226
 % identity 74
 NCBI Description (AF012833) similar to dynamin-like protein encoded by GenBank Accession Number X99669 [Arabidopsis thaliana]

Seq. No. 6515
 Contig ID 6933_2.R1040
 5'-most EST leu701152583.h1
 Method BLASTX
 NCBI GI g2576411
 BLAST score 221

E value 6.0e-18
 Match length 71
 % identity 63
 NCBI Description (AF012833) similar to dynamin-like protein encoded by
 GenBank Accession Number X99669 [Arabidopsis thaliana]

Seq. No. 6516
 Contig ID 6933_3.R1040
 5'-most EST zhf700955208.h1
 Method BLASTX
 NCBI GI g2576411
 BLAST score 329
 E value 1.0e-30
 Match length 101
 % identity 67
 NCBI Description (AF012833) similar to dynamin-like protein encoded by
 GenBank Accession Number X99669 [Arabidopsis thaliana]

Seq. No. 6517
 Contig ID 6934_1.R1040
 5'-most EST LIB3030-007-Q1-B1-G6
 Method BLASTX
 NCBI GI g1707015
 BLAST score 171
 E value 5.0e-12
 Match length 131
 % identity 32
 NCBI Description (U78721) protein phosphatase 2C isolog [Arabidopsis
 thaliana]

Seq. No. 6518
 Contig ID 6935_1.R1040
 5'-most EST zhf700963017.h1
 Method BLASTX
 NCBI GI g4468812
 BLAST score 808
 E value 2.0e-86
 Match length 221
 % identity 66
 NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 6519
 Contig ID 6937_1.R1040
 5'-most EST LIB3109-031-Q1-K1-D10
 Method BLASTX
 NCBI GI g1351651
 BLAST score 215
 E value 6.0e-17
 Match length 163
 % identity 31
 NCBI Description HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I
 >gi_2130353_pir_S62553 hypothetical protein SPAC24B11.08c
 - fission yeast (Schizosaccharomyces pombe)
 >gi_1061296_emb_CAA91773_ (Z67757) unknown
 [Schizosaccharomyces pombe]

Seq. No. 6520

% identity 41
 NCBI Description (U54559) translation initiation factor eIF3 p40 subunit
 [Homo sapiens] >gi_4503515_ref_NP_003747.1_pEIF3S3_ UNKNOWN

Seq. No. 6528
 Contig ID 6951_2.R1040
 5'-most EST kmv700738117.h1
 Method BLASTX
 NCBI GI g2351380
 BLAST score 133
 E value 7.0e-13
 Match length 149
 % identity 36
 NCBI Description (U54559) translation initiation factor eIF3 p40 subunit
 [Homo sapiens] >gi_4503515_ref_NP_003747.1_pEIF3S3_ UNKNOWN

Seq. No. 6529
 Contig ID 6952_1.R1040
 5'-most EST LIB3030-006-Q1-B1-E12
 Method BLASTX
 NCBI GI g1762584
 BLAST score 269
 E value 2.0e-23
 Match length 99
 % identity 49
 NCBI Description (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
 [Arabidopsis thaliana]

Seq. No. 6530
 Contig ID 6952_2.R1040
 5'-most EST uC-gmropic049h03b1
 Method BLASTX
 NCBI GI g1762584
 BLAST score 187
 E value 6.0e-14
 Match length 59
 % identity 59
 NCBI Description (U63373) polygalacturonase isoenzyme 1 beta subunit homolog
 [Arabidopsis thaliana]

Seq. No. 6531
 Contig ID 6956_1.R1040
 5'-most EST LIB3170-021-Q1-K1-A12

Seq. No. 6532
 Contig ID 6960_1.R1040
 5'-most EST uC-gmrominsoy066e08b1
 Method BLASTX
 NCBI GI g3182915
 BLAST score 630
 E value 2.0e-65
 Match length 180
 % identity 62
 NCBI Description ADP-RIBOSYLATION FACTOR >gi_1842150_dbj_BAA19225_
 (AB001051) ADP-ribosylation factor [Dugesia japonica]

Seq. No. 6533

Seq. No. 6552
 Contig ID 6982_1.R1040
 5'-most EST LIB3049-044-Q1-E1-G2

Seq. No. 6553
 Contig ID 6983_1.R1040
 5'-most EST gsv701053487.h1
 Method BLASTX
 NCBI GI g2275210
 BLAST score 454
 E value 5.0e-45
 Match length 175
 % identity 51
 NCBI Description (AC002337) peptidyl-prolyl cis-trans isomerase isolog
 [Arabidopsis thaliana]

Seq. No. 6554
 Contig ID 6983_2.R1040
 5'-most EST fua701043243.h1
 Method BLASTX
 NCBI GI g2275210
 BLAST score 194
 E value 8.0e-33
 Match length 174
 % identity 50
 NCBI Description (AC002337) peptidyl-prolyl cis-trans isomerase isolog
 [Arabidopsis thaliana]

Seq. No. 6555
 Contig ID 6985_1.R1040
 5'-most EST uaw700665809.h1

Seq. No. 6556
 Contig ID 6987_1.R1040
 5'-most EST g4395747
 Method BLASTN
 NCBI GI g19655
 BLAST score 466
 E value 0.0e+00
 Match length 510
 % identity 98
 NCBI Description M.sativa 26S rRNA

Seq. No. 6557
 Contig ID 6987_2.R1040
 5'-most EST zpv700760254.h1
 Method BLASTN
 NCBI GI g311302
 BLAST score 42
 E value 1.0e-13
 Match length 102
 % identity 85
 NCBI Description N.sylvestris mRNA

Seq. No. 6558
 Contig ID 6987_3.R1040
 5'-most EST asn701140057.h1

Method BLASTN
 NCBI GI g311302
 BLAST score 33
 E value 6.0e-09
 Match length 89
 % identity 84
 NCBI Description N.sylvestris mRNA

Seq. No. 6559
 Contig ID 6987_4.R1040
 5'-most EST LIB3107-029-Q1-K1-B2
 Method BLASTN
 NCBI GI g22553
 BLAST score 76
 E value 1.0e-34
 Match length 80
 % identity 99
 NCBI Description Tomato 25S ribosomal RNA gene

Seq. No. 6560
 Contig ID 6989_1.R1040
 5'-most EST rlr700896221.h1

Seq. No. 6561
 Contig ID 6991_1.R1040
 5'-most EST jC-gmst02400049e03d1

Seq. No. 6562
 Contig ID 6994_1.R1040
 5'-most EST LIB3030-007-Q1-B1-A1
 Method BLASTN
 NCBI GI g3290208
 BLAST score 51
 E value 1.0e-19
 Match length 71
 % identity 93
 NCBI Description Malus domestica MADS-box protein 1 mRNA, complete cds

Seq. No. 6563
 Contig ID 6999_1.R1040
 5'-most EST LIB3051-025-Q1-K1-F2

Seq. No. 6564
 Contig ID 6999_2.R1040
 5'-most EST LIB3107-015-Q1-K1-A2

Seq. No. 6565
 Contig ID 7001_1.R1040
 5'-most EST uC-gmropic043c05b1
 Method BLASTX
 NCBI GI g3482933
 BLAST score 1260
 E value 1.0e-139
 Match length 552
 % identity 49
 NCBI Description (AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

09684016-101000

NCBI Description Vigna radiata vacuolar H⁺-ATPase subunit A mRNA, complete cds

Seq. No. 6579
Contig ID 7020_6.R1040
5'-most EST jex700905426.h1
Method BLASTN
NCBI GI g849135
BLAST score 140
E value 5.0e-73
Match length 180
% identity 94

NCBI Description Vigna radiata vacuolar H⁺-ATPase subunit A mRNA, complete cds

Seq. No. 6580
Contig ID 7022_1.R1040
5'-most EST LIB3092-021-Q1-K1-D2
Method BLASTX
NCBI GI g4079809
BLAST score 253
E value 3.0e-21
Match length 198
% identity 3
NCBI Description (AF071172) HERC2 [Homo sapiens]

Seq. No. 6581
Contig ID 7023_1.R1040
5'-most EST jex700904926.h1
Method BLASTX
NCBI GI g3080389
BLAST score 375
E value 3.0e-72
Match length 187
% identity 74
NCBI Description (AL022603) putative membrane associated protein [Arabidopsis thaliana]

Seq. No. 6582
Contig ID 7024_1.R1040
5'-most EST pmv700894358.h1

Seq. No. 6583
Contig ID 7025_1.R1040
5'-most EST leu701145072.h1
Method BLASTX
NCBI GI g4455313
BLAST score 469
E value 6.0e-47
Match length 155
% identity 54
NCBI Description (AL035528) fatty acid elongase-like protein (cer2-like) [Arabidopsis thaliana]

Seq. No. 6584
Contig ID 7025_2.R1040
5'-most EST LIB3055-005-Q1-N1-C10

Contig ID 7060_1.R1040
 5'-most EST LIB3139-118-P1-N1-E3
 Method BLASTX
 NCBI GI g1737222
 BLAST score 2812
 E value 0.0e+00
 Match length 583
 % identity 86
 NCBI Description (U79958) BP-80 vacuolar sorting receptor [Pisum sativum]

Seq. No. 6600
 Contig ID 7060_2.R1040
 5'-most EST zhf700953252.h1
 Method BLASTX
 NCBI GI g1737222
 BLAST score 461
 E value 9.0e-46
 Match length 105
 % identity 84
 NCBI Description (U79958) BP-80 vacuolar sorting receptor [Pisum sativum]

Seq. No. 6601
 Contig ID 7060_3.R1040
 5'-most EST LIB3040-016-Q1-E1-C12
 Method BLASTX
 NCBI GI g2911587
 BLAST score 436
 E value 5.0e-43
 Match length 160
 % identity 54
 NCBI Description (AJ224442) methyltransferase [Homo sapiens]

Seq. No. 6602
 Contig ID 7060_4.R1040
 5'-most EST djj700605996.h2
 Method BLASTN
 NCBI GI g414831
 BLAST score 67
 E value 5.0e-29
 Match length 71
 % identity 99
 NCBI Description Glycine max (Rab1p) mRNA, complete cds

Seq. No. 6603
 Contig ID 7060_5.R1040
 5'-most EST LIB3109-032-Q1-K1-C2

Seq. No. 6604
 Contig ID 7061_1.R1040
 5'-most EST LIB3030-006-Q1-B1-B11

Seq. No. 6605
 Contig ID 7062_1.R1040
 5'-most EST uC-gmrominsoy060c08b1

Seq. No. 6606
 Contig ID 7062_2.R1040

E value 1.0e-111
 Match length 400
 % identity 88
 NCBI Description P.sativum PHSP1 mRNA for HSP70

 Seq. No. 6611
 Contig ID 7072_1.R1040
 5'-most EST LIB3170-034-Q1-K1-F4
 Method BLASTX
 NCBI GI g2462744
 BLAST score 291
 E value 4.0e-26
 Match length 86
 % identity 65
 NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 6612
 Contig ID 7073_1.R1040
 5'-most EST pcp700994935.h1
 Method BLASTX
 NCBI GI g1304599
 BLAST score 307
 E value 1.0e-27
 Match length 222
 % identity 26
 NCBI Description (U41315) ZNF127-Xp [Homo sapiens]

Seq. No. 6613
 Contig ID 7073_2.R1040
 5'-most EST fde700872991.h1

Seq. No. 6614
 Contig ID 7079_1.R1040
 5'-most EST LIB3170-032-Q1-K1-F3
 Method BLASTX
 NCBI GI g3021336
 BLAST score 261
 E value 2.0e-22
 Match length 122
 % identity 50
 NCBI Description (AJ224957) RGA-like [Arabidopsis thaliana]

Seq. No. 6615
 Contig ID 7079_2.R1040
 5'-most EST LIB3039-051-Q1-E1-F6
 Method BLASTX
 NCBI GI g3785986
 BLAST score 265
 E value 6.0e-23
 Match length 111
 % identity 50
 NCBI Description (AC005560) RGA1 protein [Arabidopsis thaliana]

Seq. No. 6616
 Contig ID 7080_1.R1040
 5'-most EST LIB3030-005-Q1-B1-H8

Seq. No. 6617
 Contig ID 7086_1.R1040
 5'-most EST jsh701069332.h1

Seq. No. 6618
 Contig ID 7091_1.R1040
 5'-most EST LIB3107-032-Q1-K1-C5
 Method BLASTN
 NCBI GI g4415928
 BLAST score 51
 E value 2.0e-19
 Match length 103
 % identity 87
 NCBI Description Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 6619
 Contig ID 7091_2.R1040
 5'-most EST uC-gmropic098e09b1
 Method BLASTX
 NCBI GI g4415936
 BLAST score 255
 E value 8.0e-22
 Match length 184
 % identity 36
 NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

Seq. No. 6620
 Contig ID 7099_1.R1040
 5'-most EST LIB3039-009-Q1-E1-G3
 Method BLASTX
 NCBI GI g3281861
 BLAST score 194
 E value 1.0e-14
 Match length 122
 % identity 39
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 6621
 Contig ID 7100_1.R1040
 5'-most EST jC-gmle01810056d04a1
 Method BLASTX
 NCBI GI g4115379
 BLAST score 309
 E value 3.0e-28
 Match length 101
 % identity 59
 NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No. 6622
 Contig ID 7100_2.R1040
 5'-most EST zsg701119727.h1
 Method BLASTX
 NCBI GI g4115379
 BLAST score 287
 E value 1.0e-25

Method BLASTX
 NCBI GI g1703036
 BLAST score 189
 E value 5.0e-14
 Match length 79
 % identity 47
 NCBI Description 5'-AMP-ACTIVATED PROTEIN KINASE, BETA-1 SUBUNIT (AMPK BETA-1 CHAIN) (40 KD SUBUNIT) >gi_1335858 (U42411)
 5'-AMP-activated protein kinase, beta subunit [Rattus norvegicus]

Seq. No. 6636
 Contig ID 7123_2.R1040
 5'-most EST uC-gmflminsoy026h11b1

Seq. No. 6637
 Contig ID 7124_1.R1040
 5'-most EST leu701150036.h1
 Method BLASTN
 NCBI GI g18569
 BLAST score 425
 E value 0.0e+00
 Match length 476
 % identity 100
 NCBI Description G.max coxII gene for cytochrome oxidase subunit

Seq. No. 6638
 Contig ID 7125_1.R1040
 5'-most EST LIB3030-005-Q1-B1-C9
 Method BLASTX
 NCBI GI g4263777
 BLAST score 1389
 E value 1.0e-154
 Match length 348
 % identity 70
 NCBI Description (AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No. 6639
 Contig ID 7127_1.R1040
 5'-most EST uC-gmropic037g05b1
 Method BLASTX
 NCBI GI g2344887
 BLAST score 740
 E value 2.0e-78
 Match length 223
 % identity 66
 NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 6640
 Contig ID 7127_2.R1040
 5'-most EST LIB3030-005-Q1-B1-D10

Seq. No. 6641
 Contig ID 7129_1.R1040
 5'-most EST uaw700665131.h1

Seq. No. 6648
 Contig ID 7138_1.R1040
 5'-most EST g5606078
 Method BLASTX
 NCBI GI g3023751
 BLAST score 440
 E value 2.0e-43
 Match length 100
 % identity 28
 NCBI Description 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No. 6649
 Contig ID 7139_1.R1040
 5'-most EST LIB3030-005-Q1-B1-E11
 Method BLASTX
 NCBI GI g4371285
 BLAST score 398
 E value 9.0e-39
 Match length 104
 % identity 71
 NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6650
 Contig ID 7140_1.R1040
 5'-most EST g4282509
 Method BLASTX
 NCBI GI g3702368
 BLAST score 1123
 E value 1.0e-123
 Match length 296
 % identity 68
 NCBI Description (AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]

Seq. No. 6651
 Contig ID 7141_1.R1040
 5'-most EST epX701106727.h1

Seq. No. 6652
 Contig ID 7146_1.R1040
 5'-most EST uC-gmronoir064d10b1

Seq. No. 6653
 Contig ID 7147_1.R1040
 5'-most EST fde700874693.h1
 Method BLASTX
 NCBI GI g3080437
 BLAST score 180
 E value 6.0e-13
 Match length 54
 % identity 61
 NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 6654
 Contig ID 7152_1.R1040
 5'-most EST jC-gmst02400009e02a1
 Method BLASTX
 NCBI GI g3269288
 BLAST score 800
 E value 2.0e-85
 Match length 199
 % identity 78
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 6655
 Contig ID 7153_1.R1040
 5'-most EST rca700996111.h1
 Method BLASTX
 NCBI GI g3450842
 BLAST score 624
 E value 4.0e-65
 Match length 159
 % identity 68
 NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No. 6656
 Contig ID 7154_1.R1040
 5'-most EST LIB3030-005-Q1-B1-C4
 Method BLASTX
 NCBI GI g4455192
 BLAST score 376
 E value 4.0e-36
 Match length 150
 % identity 49
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 6657
 Contig ID 7156_1.R1040
 5'-most EST xpa700792358.h1
 Method BLASTX
 NCBI GI g3142295
 BLAST score 249
 E value 4.0e-21
 Match length 94
 % identity 53
 NCBI Description (AC002411) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. [Arabidopsis thaliana]

Seq. No. 6658
 Contig ID 7156_2.R1040
 5'-most EST vzy700754349.h1
 Method BLASTX
 NCBI GI g3142295
 BLAST score 176
 E value 1.0e-12
 Match length 53
 % identity 62

NCBI Description (AC002411) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. [Arabidopsis thaliana]

Seq. No. 6659
 Contig ID 7160_1.R1040
 5'-most EST jex700905076.h1
 Method BLASTX
 NCBI GI g2924512
 BLAST score 355
 E value 1.0e-33
 Match length 91
 % identity 67

NCBI Description (AL022023) beta-galactosidase - like protein [Arabidopsis thaliana]

Seq. No. 6660
 Contig ID 7164_1.R1040
 5'-most EST uC-gmrominsoy0001h07b1

Seq. No. 6661
 Contig ID 7167_1.R1040
 5'-most EST LIB3030-005-Q1-B1-A2

Seq. No. 6662
 Contig ID 7170_1.R1040
 5'-most EST LIB3030-005-Q1-B1-A6

Seq. No. 6663
 Contig ID 7174_1.R1040
 5'-most EST zhf700962284.h1
 Method BLASTX
 NCBI GI g4467128
 BLAST score 897
 E value 6.0e-97
 Match length 228
 % identity 76
 NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 6664
 Contig ID 7176_1.R1040
 5'-most EST LIB3030-004-Q1-B1-G1
 Method BLASTX
 NCBI GI g4512652
 BLAST score 169
 E value 1.0e-11
 Match length 221
 % identity 28
 NCBI Description (AC007048) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6665
 Contig ID 7177_1.R1040
 5'-most EST uC-gmflminsoy080c10b1
 Method BLASTX
 NCBI GI g2213590
 BLAST score 421
 E value 4.0e-41

09584036.10.1000

E value 7.0e-19
Match length 105
% identity 48
NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 6672
Contig ID 7196_1.R1040
5'-most EST LIB3030-004-Q1-B1-E8

Seq. No. 6673
Contig ID 7197_1.R1040
5'-most EST leu701149726.h1

Seq. No. 6674
Contig ID 7203_1.R1040
5'-most EST LIB3040-023-Q1-E1-A12
Method BLASTN
NCBI GI g1272409
BLAST score 240
E value 1.0e-132
Match length 384
% identity 91
NCBI Description Vicia faba immunophilin precursor (FKBP15) mRNA, complete cds

Seq. No. 6675
Contig ID 7209_1.R1040
5'-most EST LIB3106-105-Q1-K1-E4
Method BLASTX
NCBI GI g2275202
BLAST score 178
E value 6.0e-13
Match length 60
% identity 60
NCBI Description (AC002337) acyl-CoA synthetase isolog [Arabidopsis thaliana]

Seq. No. 6676
Contig ID 7213_1.R1040
5'-most EST bth700843983.h1
Method BLASTX
NCBI GI g1841475
BLAST score 353
E value 2.0e-33
Match length 80
% identity 75
NCBI Description (Y11105) Myb26 [Pisum sativum]

Seq. No. 6677
Contig ID 7213_2.R1040
5'-most EST uC-gmflminsoy037e05b1
Method BLASTX
NCBI GI g1002796
BLAST score 500
E value 9.0e-51
Match length 121
% identity 74

5'-most EST ssr700559125.h1
 Method BLASTN
 NCBI GI g887572
 BLAST score 74
 E value 3.0e-33
 Match length 206
 % identity 84
 NCBI Description P.sativum mRNA for starch synthase (2988 bp)

Seq. No. 6696
 Contig ID 7245_1.R1040
 5'-most EST bth700846389.h1
 Method BLASTX
 NCBI GI g3023713
 BLAST score 642
 E value 3.0e-67
 Match length 141
 % identity 87
 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
 (U09450) enolase [Oryza sativa]

Seq. No. 6697
 Contig ID 7245_2.R1040
 5'-most EST uC-gmropic045a01b1
 Method BLASTX
 NCBI GI g3023713
 BLAST score 478
 E value 4.0e-48
 Match length 110
 % identity 85
 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
 (U09450) enolase [Oryza sativa]

Seq. No. 6698
 Contig ID 7247_1.R1040
 5'-most EST LIB3170-043-Q1-J1-G7
 Method BLASTN
 NCBI GI g4159706
 BLAST score 49
 E value 2.0e-18
 Match length 173
 % identity 82
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
 MGL6, complete sequence [Arabidopsis thaliana]

Seq. No. 6699
 Contig ID 7247_2.R1040
 5'-most EST leu701149612.h1
 Method BLASTN
 NCBI GI g4159706
 BLAST score 52
 E value 5.0e-20
 Match length 176
 % identity 82
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

Contig ID	7277_3.R1040
5'-most EST	LIB3106-072-P1-K1-G1
Method	BLASTX
NCBI GI	g3298443
BLAST score	155
E value	2.0e-10
Match length	57
% identity	61
NCBI Description	(AB010880) chloroplast ribosomal protein L17 [Nicotiana tabacum]
Seq. No.	6721
Contig ID	7278_2.R1040
5'-most EST	LIB3030-003-Q1-B1-D12
Seq. No.	6722
Contig ID	7280_1.R1040
5'-most EST	LIB3030-003-Q1-B1-D5
Method	BLASTX
NCBI GI	g4206122
BLAST score	419
E value	3.0e-41
Match length	146
% identity	60
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]
Seq. No.	6723
Contig ID	7281_1.R1040
5'-most EST	uC-gmropic050b08b1
Method	BLASTX
NCBI GI	g399333
BLAST score	489
E value	2.0e-49
Match length	128
% identity	75
NCBI Description	CYSTEINE SYNTHASE CHLOROPLAST PRECURSOR (O-ACETYL SERINE SULFHYDRYLASE) (O-ACETYL SERINE (THIOL)-LYASE) (CSASE) >gi_322740_pir_A43407 cysteine synthase (EC 4.2.99.8) precursor - pepper >gi_17944_emb_CAA46086_ (X64874) O-acetylserine (thiol)-lyase [Capsicum annuum]
Seq. No.	6724
Contig ID	7281_2.R1040
5'-most EST	LIB3030-003-Q1-B1-D7
Seq. No.	6725
Contig ID	7286_1.R1040
5'-most EST	jC-gmle01810055g05a1
Method	BLASTX
NCBI GI	g4006865
BLAST score	817
E value	2.0e-87
Match length	227
% identity	67
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 6726
 Contig ID 7286_3.R1040
 5'-most EST zpv700761628.h1
 Method BLASTX
 NCBI GI g2190551
 BLAST score 163
 E value 2.0e-11
 Match length 39
 % identity 85
 NCBI Description (AC001229) Similar to C. elegans hypothetical protein K07C5.6 (gb_Z71181). ESTs gb_H36844, gb_AA394956 come from this gene. [Arabidopsis thaliana]

Seq. No. 6727
 Contig ID 7287_1.R1040
 5'-most EST leu701147472.h1
 Method BLASTX
 NCBI GI g541944
 BLAST score 632
 E value 1.0e-65
 Match length 181
 % identity 71
 NCBI Description nodulin-26 - soybean

Seq. No. 6728
 Contig ID 7287_2.R1040
 5'-most EST asn701134248.h1
 Method BLASTX
 NCBI GI g1076748
 BLAST score 379
 E value 8.0e-37
 Match length 93
 % identity 77
 NCBI Description major intrinsic protein - rice >gi_440869_dbj_BAA04257_ (D17443) major intrinsic protein [Oryza sativa]

Seq. No. 6729
 Contig ID 7289_1.R1040
 5'-most EST bnh700764511.h1
 Method BLASTX
 NCBI GI g1076668
 BLAST score 650
 E value 4.0e-68
 Match length 158
 % identity 79
 NCBI Description NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No. 6730
 Contig ID 7289_2.R1040
 5'-most EST leu701151520.h1
 Method BLASTX
 NCBI GI g1076668
 BLAST score 153
 E value 2.0e-10
 Match length 62

BLAST score	38
E value	6.0e-12
Match length	94
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	6744
Contig ID	7308_1.R1040
5'-most EST	LIB3049-037-Q1-E1-F1
Method	BLASTX
NCBI GI	g4235430
BLAST score	752
E value	1.0e-147
Match length	418
% identity	64
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]
Seq. No.	6745
Contig ID	7308_2.R1040
5'-most EST	fde700875009.h1
Method	BLASTX
NCBI GI	g4235430
BLAST score	748
E value	2.0e-79
Match length	231
% identity	65
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]
Seq. No.	6746
Contig ID	7315_1.R1040
5'-most EST	uC-gmrominsoy200b02b1
Method	BLASTX
NCBI GI	g2827529
BLAST score	793
E value	1.0e-84
Match length	304
% identity	53
NCBI Description	(AL021633) putative protein [Arabidopsis thaliana]
Seq. No.	6747
Contig ID	7317_1.R1040
5'-most EST	LIB3049-052-Q1-E1-H5
Seq. No.	6748
Contig ID	7319_1.R1040
5'-most EST	hrw701057579.h1
Method	BLASTX
NCBI GI	g2244898
BLAST score	327
E value	4.0e-30
Match length	201
% identity	48
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]
Seq. No.	6749

Method BLASTX
 NCBI GI g2213610
 BLAST score 146
 E value 1.0e-09
 Match length 47
 % identity 32
 NCBI Description (AC000103) F21J9.4 [Arabidopsis thaliana]

Seq. No. 6754
 Contig ID 7324_7.R1040
 5'-most EST zhf700961396.h1
 Method BLASTN
 NCBI GI g20732
 BLAST score 43
 E value 4.0e-15
 Match length 63
 % identity 92
 NCBI Description Pea chloroplast GAPB mRNA encoding
 glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit B
 (EC 1.2.1.13)

Seq. No. 6755
 Contig ID 7326_1.R1040
 5'-most EST LIB3039-015-Q1-E1-E2
 Method BLASTX
 NCBI GI g4218120
 BLAST score 739
 E value 2.0e-99
 Match length 260
 % identity 72
 NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis
 thaliana]

Seq. No. 6756
 Contig ID 7327_1.R1040
 5'-most EST LIB3092-007-Q1-K1-D7

Seq. No. 6757
 Contig ID 7331_1.R1040
 5'-most EST jex700904224.h1
 Method BLASTX
 NCBI GI g2505940
 BLAST score 551
 E value 1.0e-56
 Match length 130
 % identity 82
 NCBI Description (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]

Seq. No. 6758
 Contig ID 7331_2.R1040
 5'-most EST LIB3087-012-Q1-K1-G3
 Method BLASTX
 NCBI GI g2505940
 BLAST score 387
 E value 2.0e-37
 Match length 103
 % identity 77

% identity 48
NCBI Description (U94784) unconventional myosin [*Helianthus annuus*]

Seq. No. 6773
Contig ID 7369_1.R1040
5'-most EST LIB3106-054-Q1-K1-E10
Method BLASTX
NCBI GI g2961346
BLAST score 387
E value 2.0e-37
Match length 96
% identity 70
NCBI Description (AL022140) pectinesterase like protein [*Arabidopsis thaliana*]

Seq. No. 6774
Contig ID 7370_1.R1040
5'-most EST trc700566871.h1
Method BLASTX
NCBI GI g173419
BLAST score 253
E value 2.0e-36
Match length 118
% identity 67
NCBI Description (L11574) p68 RNA helicase [*Schizosaccharomyces pombe*]
>gi_3810840_emb_CAA21801_ (AL032684) p68-like protein.
[*Schizosaccharomyces pombe*]

Seq. No. 6775
Contig ID 7376_1.R1040
5'-most EST LIB3030-001-Q1-B1-H4
Method BLASTX
NCBI GI g2459438
BLAST score 248
E value 5.0e-21
Match length 133
% identity 51
NCBI Description (AC002332) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 6776
Contig ID 7377_1.R1040
5'-most EST LIB3030-001-Q1-B1-H5

Seq. No. 6777
Contig ID 7378_1.R1040
5'-most EST LIB3092-044-Q1-K1-E3
Method BLASTX
NCBI GI g2257756
BLAST score 450
E value 3.0e-44
Match length 302
% identity 39
NCBI Description (U82815) nucleolar histone deacetylase HD2-p39 [*Zea mays*]
>gi_3650466 (AF026917) histone deacetylase HD2-p39 [*Zea mays*]

Seq. No. 6778

Seq. No. 6796
 Contig ID 7397_1.R1040
 5'-most EST LIB3030-001-Q1-B1-G12
 Method BLASTX
 NCBI GI g2129740
 BLAST score 300
 E value 8.0e-27
 Match length 105
 % identity 59
 NCBI Description small nuclear ribonucleoprotein - Arabidopsis thaliana
 >gi_2129756_pir_S71411 U1 snRNP 70K protein - Arabidopsis
 thaliana >gi_1255711 (M93439) small nuclear
 ribonucleoprotein [Arabidopsis thaliana] >gi_1354469
 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]

Seq. No. 6797
 Contig ID 7397_2.R1040
 5'-most EST jC-gmro02910048h03a1
 Method BLASTX
 NCBI GI g2129740
 BLAST score 388
 E value 6.0e-38
 Match length 88
 % identity 81
 NCBI Description small nuclear ribonucleoprotein - Arabidopsis thaliana
 >gi_2129756_pir_S71411 U1 snRNP 70K protein - Arabidopsis
 thaliana >gi_1255711 (M93439) small nuclear
 ribonucleoprotein [Arabidopsis thaliana] >gi_1354469
 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]

Seq. No. 6798
 Contig ID 7398_1.R1040
 5'-most EST fC-gmro7000748475f1
 Method BLASTX
 NCBI GI g3820531
 BLAST score 592
 E value 3.0e-61
 Match length 169
 % identity 63
 NCBI Description (AF072736) beta-glucosidase [Pinus contorta]

Seq. No. 6799
 Contig ID 7401_1.R1040
 5'-most EST epX701106660.h1
 Method BLASTX
 NCBI GI g1946359
 BLAST score 361
 E value 2.0e-34
 Match length 89
 % identity 73
 NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 6800
 Contig ID 7403_1.R1040
 5'-most EST hrw701060631.h1
 Method BLASTN

5'-most EST LIB3170-067-Q1-K1-E8
 Method BLASTX
 NCBI GI g729668
 BLAST score 348
 E value 2.0e-32
 Match length 136
 % identity 56
 NCBI Description HISTONE H1 >gi_2147479_pir_S65059 histone H1,
 drought-inducible - Lycopersicon pennellii >gi_436823
 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No. 6807
 Contig ID 7410_1.R1040
 5'-most EST LIB3106-062-Q1-K1-G9
 Method BLASTX
 NCBI GI g2642158
 BLAST score 324
 E value 1.0e-52
 Match length 136
 % identity 71
 NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6808
 Contig ID 7410_2.R1040
 5'-most EST uaw700663338.h1

Seq. No. 6809
 Contig ID 7411_1.R1040
 5'-most EST LIB3030-001-Q1-B1-E12
 Method BLASTX
 NCBI GI g2924509
 BLAST score 666
 E value 9.0e-70
 Match length 229
 % identity 54
 NCBI Description (AL022023) subtilisin proteinase - like [Arabidopsis thaliana]

Seq. No. 6810
 Contig ID 7412_1.R1040
 5'-most EST vwf700676026.h1

Seq. No. 6811
 Contig ID 7413_1.R1040
 5'-most EST LIB3030-001-Q1-B1-E3
 Method BLASTX
 NCBI GI g3738339
 BLAST score 314
 E value 2.0e-28
 Match length 123
 % identity 54
 NCBI Description (AC005170) putative kinase [Arabidopsis thaliana]

Seq. No. 6812
 Contig ID 7413_2.R1040
 5'-most EST LIB3049-006-Q1-E1-C6


```

BLAST score                227
E value                    9.0e-19
Match length              57
% identity                81
NCBI Description          (AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.                  6827
Contig ID                 7430_1.R1040
5'-most EST              jex700904532.h1

Seq. No.                  6828
Contig ID                 7433_1.R1040
5'-most EST              g4290321

Seq. No.                  6829
Contig ID                 7442_1.R1040
5'-most EST              LIB3040-040-Q1-E1-B3
Method                   BLASTX
NCBI GI                   g2135841
BLAST score              184
E value                  7.0e-13
Match length             78
% identity               46
NCBI Description          nucleic acid-binding protein E5.1 - human >gi_598231
                          (L37368) RNA-binding protein [Homo sapiens]

Seq. No.                  6830
Contig ID                 7448_1.R1040
5'-most EST              LIB3030-001-Q1-B1-B5
Method                   BLASTX
NCBI GI                   g3915022
BLAST score              768
E value                  5.0e-82
Match length             178
% identity               83
NCBI Description          SUCROSE-PHOSPHATE SYNTHASE 2
                          (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE
                          >gi_2190350_emb_CAA72491_ (Y11795) sucrose-phosphate
                          synthase [Craterostigma plantagineum]

Seq. No.                  6831
Contig ID                 7449_1.R1040
5'-most EST              g5606523

Seq. No.                  6832
Contig ID                 7450_1.R1040
5'-most EST              LIB3106-101-Q1-K1-F9
Method                   BLASTX
NCBI GI                   g3915665
BLAST score              236
E value                  3.0e-27
Match length             143
% identity               44
NCBI Description          ELONGATION FACTOR G (EF-G) >gi_2688449 (AE001155)
                          translation elongation factor G (fus-1) [Borrelia
                          burgdorferi]

```


% identity 83
 NCBI Description (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No. 6839
 Contig ID 7466_2.R1040
 5'-most EST pmv700893276.h1
 Method BLASTN
 NCBI GI g3107930
 BLAST score 99
 E value 4.0e-48
 Match length 316
 % identity 83

NCBI Description Pyrus pyrifolia mRNA for UDP-glucose pyrophosphorylase, complete cds

Seq. No. 6840
 Contig ID 7466_3.R1040
 5'-most EST jC-gmst02400062h08d1
 Method BLASTX
 NCBI GI g136739
 BLAST score 232
 E value 3.0e-19
 Match length 59
 % identity 75

NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir_XNPOU
 UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No. 6841
 Contig ID 7466_5.R1040
 5'-most EST pxt700946288.h1
 Method BLASTX
 NCBI GI g3107931
 BLAST score 175
 E value 1.0e-12
 Match length 43
 % identity 72

NCBI Description (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No. 6842
 Contig ID 7466_9.R1040
 5'-most EST ncj700981983.h1
 Method BLASTX
 NCBI GI g136739
 BLAST score 123
 E value 3.0e-14
 Match length 55
 % identity 80

NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir_XNPOU
 UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No. 6843

09634016-1010000

E value 2.0e-14
Match length 62
% identity 55
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 6891
Contig ID 7538_1.R1040
5'-most EST fC-gmro700797913a1
Method BLASTX
NCBI GI g2627181
BLAST score 682
E value 6.0e-72
Match length 153
% identity 80
NCBI Description (D89619) cycloartenol synthase [Pisum sativum]

Seq. No. 6892
Contig ID 7540_1.R1040
5'-most EST epX701107112.h1
Method BLASTX
NCBI GI g4454471
BLAST score 685
E value 8.0e-72
Match length 315
% identity 48
NCBI Description (AC006234) putative G protein coupled receptor [Arabidopsis thaliana]

Seq. No. 6893
Contig ID 7541_1.R1040
5'-most EST LIB3030-009-Q1-B1-C4
Method BLASTX
NCBI GI g3522950
BLAST score 228
E value 1.0e-18
Match length 99
% identity 49
NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6894
Contig ID 7545_1.R1040
5'-most EST LIB3030-009-Q1-B1-E1

Seq. No. 6895
Contig ID 7551_1.R1040
5'-most EST kl1701207181.h1
Method BLASTN
NCBI GI g1044939
BLAST score 226
E value 1.0e-124
Match length 432
% identity 91
NCBI Description Z.mays mRNA for ubiquitin/ribosomal protein S27a fusion protein

Seq. No. 6896
Contig ID 7551_3.R1040

0964015

00684016.101000

Match length 203
% identity 57
NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No. 6918
Contig ID 7583 1.R1040
5'-most EST LIB3040-014-Q1-E1-E10
Method BLASTX
NCBI GI g3122386
BLAST score 1798
E value 0.0e+00
Match length 356
% identity 91
NCBI Description WD-40 REPEAT PROTEIN MSI1 >gi_2394227 (AF016845) WD-40 repeat protein [Lycopersicon esculentum]

Seq. No. 6919
Contig ID 7583 2.R1040
5'-most EST epw701106768.h1

Seq. No. 6920
Contig ID 7583 3.R1040
5'-most EST hrw701063160.h1

Seq. No. 6921
Contig ID 7583 4.R1040
5'-most EST LIB3109-029-Q1-K1-G10

Seq. No. 6922
Contig ID 7586 1.R1040
5'-most EST LIB3030-012-Q1-B1-A2
Method BLASTX
NCBI GI g4218120
BLAST score 757
E value 1.0e-85
Match length 219
% identity 70
NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No. 6923
Contig ID 7586 2.R1040
5'-most EST wrq700790986.h1
Method BLASTX
NCBI GI g4218120
BLAST score 321
E value 7.0e-30
Match length 84
% identity 70
NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No. 6924
Contig ID 7591 1.R1040
5'-most EST LIB3030-012-Q1-B1-D1

Seq. No. 6925

Seq. No. 6948
 Contig ID 7634_1.R1040
 5'-most EST epX701108179.h1
 Method BLASTX
 NCBI GI g4455293
 BLAST score 211
 E value 1.0e-16
 Match length 57
 % identity 72
 NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 6949
 Contig ID 7636_1.R1040
 5'-most EST LIB3039-054-Q1-E1-B6

Seq. No. 6950
 Contig ID 7637_1.R1040
 5'-most EST LIB3049-016-Q1-E1-F11

Seq. No. 6951
 Contig ID 7637_2.R1040
 5'-most EST LIB3093-010-Q1-K1-C1

Seq. No. 6952
 Contig ID 7638_1.R1040
 5'-most EST LIB3039-010-Q1-E1-D2

Seq. No. 6953
 Contig ID 7638_2.R1040
 5'-most EST ncj700981237.h1

Seq. No. 6954
 Contig ID 7643_1.R1040
 5'-most EST LIB3106-073-Q1-K1-C6
 Method BLASTX
 NCBI GI g4263782
 BLAST score 146
 E value 5.0e-09
 Match length 47
 % identity 53
 NCBI Description (AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6955
 Contig ID 7645_1.R1040
 5'-most EST jsh701067491.h1

Seq. No. 6956
 Contig ID 7647_1.R1040
 5'-most EST LIB3049-046-Q1-E1-F3
 Method BLASTX
 NCBI GI g3341443
 BLAST score 376
 E value 4.0e-36
 Match length 130
 % identity 57
 NCBI Description (AJ223074) acid phosphatase [Glycine max]

Contig ID 7657_3.R1040
 5'-most EST jsh701070119.h1
 Method BLASTN
 NCBI GI g3947720
 BLAST score 66
 E value 1.0e-28
 Match length 182
 % identity 84
 NCBI Description Prunus persica mRNA for ribosomal protein S28 (rps28.2)

Seq. No. 6964
 Contig ID 7657_4.R1040
 5'-most EST LIB3049-049-Q1-E1-E3
 Method BLASTX
 NCBI GI g3947719
 BLAST score 237
 E value 1.0e-19
 Match length 51
 % identity 92
 NCBI Description (AJ012653) ribosomal protein S28 [Prunus persica]
 >gi_3947721_emb_CAA10102_ (AJ012654) ribosomal protein S28
 [Prunus persica] >gi_3947723_emb_CAA10103_ (AJ012655)
 ribosomal protein S28 [Prunus persica]

Seq. No. 6965
 Contig ID 7657_7.R1040
 5'-most EST gsv701050725.h1
 Method BLASTX
 NCBI GI g3947719
 BLAST score 229
 E value 7.0e-19
 Match length 51
 % identity 88
 NCBI Description (AJ012653) ribosomal protein S28 [Prunus persica]
 >gi_3947721_emb_CAA10102_ (AJ012654) ribosomal protein S28
 [Prunus persica] >gi_3947723_emb_CAA10103_ (AJ012655)
 ribosomal protein S28 [Prunus persica]

Seq. No. 6966
 Contig ID 7659_1.R1040
 5'-most EST LIB3170-051-Q1-K2-F2
 Method BLASTX
 NCBI GI g4510379
 BLAST score 387
 E value 5.0e-37
 Match length 182
 % identity 48
 NCBI Description (AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No. 6967
 Contig ID 7665_1.R1040
 5'-most EST LIB3170-034-Q1-K1-H12
 Method BLASTN
 NCBI GI g19572
 BLAST score 150
 E value 2.0e-78
 Match length 230

NCBI Description (AC004667) putative DAL1 protein [Arabidopsis thaliana]

Seq. No. 6988
Contig ID 7684_2.R1040
5'-most EST LIB3039-033-Q1-E1-D9
Method BLASTX
NCBI GI g2459425
BLAST score 300
E value 4.0e-27
Match length 90
% identity 67

NCBI Description (AC002332) plastid protein [Arabidopsis thaliana]

Seq. No. 6989
Contig ID 7690_1.R1040
5'-most EST LIB3073-023-Q1-K1-G9
Method BLASTX
NCBI GI g294060
BLAST score 192
E value 3.0e-14
Match length 127
% identity 33

NCBI Description (L06467) major latex protein [Papaver somniferum]

Seq. No. 6990
Contig ID 7691_1.R1040
5'-most EST LIB3039-053-Q1-E1-E8
Method BLASTX
NCBI GI g99755
BLAST score 341
E value 4.0e-32
Match length 128
% identity 53

NCBI Description RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Tal-1 (fragment)
>gi_16356_emb_CAA37917_ (X53973) reverse transcriptase [Arabidopsis thaliana]

Seq. No. 6991
Contig ID 7692_1.R1040
5'-most EST LIB3039-053-Q1-E1-C1
Method BLASTX
NCBI GI g4185140
BLAST score 410
E value 4.0e-40
Match length 88
% identity 92

NCBI Description (AC005724) putative small nuclear ribonucleoprotein E (snRNP-E) [Arabidopsis thaliana]

Seq. No. 6992
Contig ID 7692_2.R1040
5'-most EST LIB3072-008-Q1-E1-E1
Method BLASTX
NCBI GI g4185140
BLAST score 409
E value 4.0e-40

Match length 88
 % identity 91
 NCBI Description (AC005724) putative small nuclear ribonucleoprotein E
 (snRNP-E) [Arabidopsis thaliana]

Seq. No. 6993
 Contig ID 7692_3.R1040
 5'-most EST LIB3170-080-Q1-K1-A12
 Method BLASTX
 NCBI GI g4185140
 BLAST score 378
 E value 2.0e-36
 Match length 81
 % identity 93
 NCBI Description (AC005724) putative small nuclear ribonucleoprotein E
 (snRNP-E) [Arabidopsis thaliana]

Seq. No. 6994
 Contig ID 7696_1.R1040
 5'-most EST LIB3056-003-Q1-N1-G2
 Method BLASTX
 NCBI GI g1730035
 BLAST score 231
 E value 7.0e-19
 Match length 121
 % identity 40
 NCBI Description PROTEIN KE2 >gi_2137410_pir_I53651 hydrophilic protein -
 mouse >gi_198574 (M65255) hydrophilic protein [Mus
 musculus] >gi_198576 (M65256) hydrophilic protein [Mus
 musculus] >gi_3811379 (AF100956) KE2 [Mus musculus]
 >gi_4050102 (AF110520) KE2 [Mus musculus]

Seq. No. 6995
 Contig ID 7696_2.R1040
 5'-most EST 6HC-01-Q1-B1-B12
 Method BLASTX
 NCBI GI g2344898
 BLAST score 571
 E value 1.0e-58
 Match length 168
 % identity 65
 NCBI Description (AC002388) 60S ribosomal protein L30 isolog [Arabidopsis
 thaliana]

Seq. No. 6996
 Contig ID 7698_1.R1040
 5'-most EST LIB3039-053-Q1-E1-C8

Seq. No. 6997
 Contig ID 7699_1.R1040
 5'-most EST LIB3040-018-Q1-E1-G4
 Method BLASTX
 NCBI GI g2431771
 BLAST score 248
 E value 7.0e-21
 Match length 114
 % identity 49

Seq. No.	7003
Contig ID	7700_3.R1040
5'-most EST	LIB3049-032-Q1-E1-A9
Method	BLASTN
NCBI GI	g3175989
BLAST score	147
E value	7.0e-77
Match length	294
% identity	88
NCBI Description	Cicer arietinum mRNA for GDP dissociation inhibitor (qdi)

```
Seq. No.          7004
Contig ID         7704_1.R1040
5'-most EST      LIB3073-024-Q1-K1-H9
```

```
Seq. No.          7005
Contig ID         7706_1.R1040
5'-most EST      LIB3065-001-Q1-N1-G12
Method            BLASTX
NCBI GI           g4263521
BLAST score       351
E value           3.0e-33
Match length      87
% identity        15
NCBI Description  (AC004044) putative WD-repeat protein [Arabidopsis
                  thaliana]
```

Seq. No.	7006
Contig ID	7708_1.R1040
5'-most EST	LIB3039-053-Q1-E1-B3

Seq. No.	7007
Contig ID	7713_1.R1040
5'-most EST	LIB3039-041-Q1-E1-C12

```
Seq. No.          7008
Contig.ID         7715_1.R1040
5'-most EST      uC-gmflminsoy077b08b1
Method            BLASTX
NCBI GI           g3785986
BLAST score       154
E value           7.0e-10
Match length      65
% identity        51
NCBI Description  (AC005560) RGA1 protein [Arabidopsis thaliana]
```

```
Seq. No.          7009
Contig ID         7727_1.R1040
5'-most EST      fC-gmse700753078a2
Method            BLASTX
NCBI GI           g3702326
BLAST score       839
E value           7.0e-90
Match length      194
% identity        81
NCBI Description  (AC005397) hypothetical protein [Arabidopsis thaliana]
```


5'-most EST sat701006613.h1

Seq. No. 7030
Contig ID 7809_1.R1040
5'-most EST leu701150109.h1

Seq. No. 7031
Contig ID 7811_1.R1040
5'-most EST leu701146266.h1

Seq. No. 7032
Contig ID 7811_2.R1040
5'-most EST ncj700978210.h1

Seq. No. 7033
Contig ID 7812_1.R1040
5'-most EST LIB3039-020-Q1-E1-B8
Method BLASTX
NCBI GI g1708464
BLAST score 257
E value 3.0e-22
Match length 90
% identity 57
NCBI Description PUTATIVE DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD)
(2,3-DIHYDROXY ACID HYDROLYASE) >gi_1213255_emb_CAA93689_
(Z69795) unknown [Schizosaccharomyces pombe]

Seq. No. 7034
Contig ID 7814_1.R1040
5'-most EST leu701144777.h1
Method BLASTX
NCBI GI g400649
BLAST score 145
E value 8.0e-09
Match length 65
% identity 40
NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 12 KD SUBUNIT PRECURSOR
(COMPLEX I-12KD) (CI-12KD) >gi_479205_pir_S32568 gene
NUO-12.3 protein - Neurospora crassa >gi_3040_emb_CAA48768_
(X68965) NUO-12.3 [Neurospora crassa]

Seq. No. 7035
Contig ID 7815_1.R1040
5'-most EST uxk700670174.h1

Seq. No. 7036
Contig ID 7820_1.R1040
5'-most EST LIB3039-051-Q1-E1-B9
Method BLASTX
NCBI GI g2827888
BLAST score 594
E value 2.0e-61
Match length 197
% identity 62
NCBI Description (AF016621) ATP-dependent Clp protease proteolytic subunit
[Arabidopsis thaliana]

Contig ID 7868_1.R1040
 5'-most EST LIB3093-035-Q1-K1-A8
 Method BLASTX
 NCBI GI g3063454
 BLAST score 148
 E value 4.0e-09
 Match length 136
 % identity 46
 NCBI Description (AC003981) F22013.16 [Arabidopsis thaliana]

Seq. No. 7050
 Contig ID 7868_2.R1040
 5'-most EST kmv700739710.h1

Seq. No. 7051
 Contig ID 7875_1.R1040
 5'-most EST awf700839764.h1
 Method BLASTX
 NCBI GI g4567302
 BLAST score 148
 E value 4.0e-09
 Match length 86
 % identity 45
 NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

Seq. No. 7052
 Contig ID 7877_1.R1040
 5'-most EST gsv701047796.h1
 Method BLASTX
 NCBI GI g2497543
 BLAST score 2263
 E value 0.0e+00
 Match length 493
 % identity 89
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir_S41379
 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_
 (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No. 7053
 Contig ID 7877_2.R1040
 5'-most EST jC-gmst02400055d10a1
 Method BLASTX
 NCBI GI g4033431
 BLAST score 570
 E value 8.0e-59
 Match length 126
 % identity 87
 NCBI Description PROBABLE PYRUVATE KINASE, CYTOSOLIC ISOZYME (PK)
 >gi_2982467_emb_CAA18231_(AL022223) pyruvate kinase like
 protein [Arabidopsis thaliana]

Seq. No. 7054
 Contig ID 7877_3.R1040
 5'-most EST LIB3170-061-Q1-K2-D11
 Method BLASTX
 NCBI GI g2497543
 BLAST score 495

E value 5.0e-50
 Match length 104
 % identity 89
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir_S41379
 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_
 (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No. 7055
 Contig ID 7877_4.R1040
 5'-most EST sat701010766.h1
 Method BLASTX
 NCBI GI g2497543
 BLAST score 436
 E value 6.0e-43
 Match length 143
 % identity 75
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir_S41379
 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_
 (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No. 7056
 Contig ID 7880_1.R1040
 5'-most EST leu701146874.h1

Seq. No. 7057
 Contig ID 7880_2.R1040
 5'-most EST LIB3170-012-Q1-J1-C11

Seq. No. 7058
 Contig ID 7883_1.R1040
 5'-most EST taw700655766.h1

Seq. No. 7059
 Contig ID 7883_2.R1040
 5'-most EST g5510176

Seq. No. 7060
 Contig ID 7883_3.R1040
 5'-most EST LIB3073-015-Q1-K1-B1

Seq. No. 7061
 Contig ID 7883_4.R1040
 5'-most EST ssr700557657.h1

Seq. No. 7062
 Contig ID 7884_1.R1040
 5'-most EST LIB3039-049-Q1-E1-H9
 Method BLASTX
 NCBI GI g4204294
 BLAST score 202
 E value 7.0e-16
 Match length 71
 % identity 66
 NCBI Description (AC003027) lcl_prt_seq No definition line found
 [Arabidopsis thaliana]

Seq. No. 7063

00000000000000000000000000000000

NCBI Description (Z98531) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 7078
Contig ID 7919_2.R1040
5'-most EST leu701155674.h1

Seq. No. 7079
Contig ID 7922_1.R1040
5'-most EST LIB3039-049-Q1-E1-D11
Method BLASTX
NCBI GI g1708971
BLAST score 381
E value 2.0e-36
Match length 160
% identity 43

NCBI Description (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
(HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
>gi_421871_pir_S32156 mandelonitrile lyase (EC 4.1.2.10) -
black cherry >gi_288116_emb_CAA51194_ (X72617)
mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814)
(R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus
serotina] >gi_1090776_prf_2019441A mandelonitrile lyase
[Prunus serotina]

Seq. No. 7080
Contig ID 7934_1.R1040
5'-most EST LIB3039-049-Q1-E1-C11
Method BLASTX
NCBI GI g416731
BLAST score 141
E value 7.0e-09
Match length 67
% identity 40

NCBI Description POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi_82655_pir_JQ1107
18.3K protein precursor, pollen - maize
>gi_255569_bbs_113677 (S44171) pollen specific protein [Zea
mays=corn, Peptide, 170 aa] [Zea mays]
>gi_1588669_prf_2209273A Zm13 [Zea mays]

Seq. No. 7081
Contig ID 7938_1.R1040
5'-most EST ncj700983184.h1
Method BLASTX
NCBI GI g1653702
BLAST score 275
E value 3.0e-24
Match length 81
% identity 68

NCBI Description (D90915) dihydrolipoamide acetyltransferase component (E2)
of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No. 7082
Contig ID 7938_2.R1040
5'-most EST uC-gmropic073g06b1
Method BLASTX
NCBI GI g1653702
BLAST score 211

NCBI Description (AF013294) contains region of similarity to SYT
[Arabidopsis thaliana]

Seq. No. 7089
Contig ID 7955_2.R1040
5'-most EST ncj700978551.h1
Method BLASTX
NCBI GI g2252866
BLAST score 266
E value 4.0e-23
Match length 56
% identity 95

NCBI Description (AF013294) contains region of similarity to SYT
[Arabidopsis thaliana]

Seq. No. 7090
Contig ID 7957_1.R1040
5'-most EST LIB3039-048-Q1-E1-F6
Method BLASTX
NCBI GI g4467111
BLAST score 173
E value 5.0e-12
Match length 63
% identity 60

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 7091
Contig ID 7961_1.R1040
5'-most EST LIB3039-048-Q1-E1-E5

Seq. No. 7092
Contig ID 7961_2.R1040
5'-most EST gsv701048205.h1

Seq. No. 7093
Contig ID 7964_1.R1040
5'-most EST uC-gmropic113a06b1
Method BLASTX
NCBI GI g729704
BLAST score 339
E value 3.0e-31
Match length 223
% identity 12

NCBI Description DNA-BINDING PROTEIN HEXBP (HEXAMER-BINDING PROTEIN)
>gi_1078700_pir_A47156 hexamer-binding protein HEXBP -
Leishmania major >gi_159342 (M94390) HEXBP DNA binding
protein [Leishmania major]

Seq. No. 7094
Contig ID 7975_1.R1040
5'-most EST LIB3039-048-Q1-E1-C6
Method BLASTX
NCBI GI g2341024
BLAST score 254
E value 5.0e-22
Match length 84
% identity 56

NCBI Description (AC000104) F19P19.1 [Arabidopsis thaliana]

Seq. No. 7095
Contig ID 7979_1.R1040
5'-most EST fC-gmle700557018f3
Method BLASTX
NCBI GI g1351271
BLAST score 1246
E value 1.0e-137
Match length 270
% identity 87
NCBI Description TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
>gi_1084309_pir_S52032 triose-phosphate isomerase (EC
5.3.1.1) precursor, chloroplast - spinach >gi_806312
(L36387) triosephosphate isomerase, chloroplast isozyme
[Spinacia oleracea]

Seq. No. 7096
Contig ID 7979_2.R1040
5'-most EST LIB3040-059-Q1-E1-H10
Method BLASTX
NCBI GI g1351271
BLAST score 701
E value 5.0e-74
Match length 182
% identity 76
NCBI Description TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
>gi_1084309_pir_S52032 triose-phosphate isomerase (EC
5.3.1.1) precursor, chloroplast - spinach >gi_806312
(L36387) triosephosphate isomerase, chloroplast isozyme
[Spinacia oleracea]

Seq. No. 7097
Contig ID 7979_3.R1040
5'-most EST fC-gmle7000739771d1
Method BLASTX
NCBI GI g1351271
BLAST score 347
E value 1.0e-32
Match length 78
% identity 87
NCBI Description TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
>gi_1084309_pir_S52032 triose-phosphate isomerase (EC
5.3.1.1) precursor, chloroplast - spinach >gi_806312
(L36387) triosephosphate isomerase, chloroplast isozyme
[Spinacia oleracea]

Seq. No. 7098
Contig ID 7979_4.R1040
5'-most EST LIB3107-068-Q1-K1-G9
Method BLASTX
NCBI GI g1174745
BLAST score 192
E value 1.0e-14
Match length 41
% identity 83
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)

>gi_1363523_pir_S53761 triose-phosphate isomerase (EC
5.3.1.1) precursor, chloroplast - rye
>gi_609262_emb_CAA83533_(Z32521) triosephosphate isomerase
[Secale cereale] >gi_1095494_prf_2109226B triosephosphate
isomerase [Secale cereale]

Seq. No. 7099
Contig ID 7989_1.R1040
5'-most EST LIB3039-048-Q1-E1-B11
Method BLASTX
NCBI GI g3080450
BLAST score 575
E value 3.0e-59
Match length 187
% identity 60
NCBI Description (AL022605) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7100
Contig ID 7995_1.R1040
5'-most EST LIB3040-055-Q1-E1-E8

Seq. No. 7101
Contig ID 7996_1.R1040
5'-most EST LIB3039-047-Q1-E1-G4

Seq. No. 7102
Contig ID 7997_1.R1040
5'-most EST leu701145158.h1
Method BLASTX
NCBI GI g3687243
BLAST score 251
E value 3.0e-21
Match length 61
% identity 80
NCBI Description (AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No. 7103
Contig ID 7997_2.R1040
5'-most EST sat701002975.h1
Method BLASTX
NCBI GI g3687243
BLAST score 146
E value 5.0e-09
Match length 32
% identity 91
NCBI Description (AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No. 7104
Contig ID 8002_1.R1040
5'-most EST LIB3039-047-Q1-E1-H2
Method BLASTX
NCBI GI g1071924
BLAST score 147
E value 1.0e-12
Match length 72

% identity 61
 NCBI Description Kunitz trypsin inhibitor precursor - soybean
 >gi_510515_emb_CAA56343_ (X80039) Kunitz trypsin inhibitor
 [Glycine max]

Seq. No. 7105
 Contig ID 8004_1.R1040
 5'-most EST LIB3039-047-Q1-E1-H7
 Method BLASTX
 NCBI GI g3747050
 BLAST score 491
 E value 2.0e-49
 Match length 118
 % identity 81
 NCBI Description (AF093540) ribosomal protein L26 [Zea mays]

Seq. No. 7106
 Contig ID 8004_2.R1040
 5'-most EST LIB3170-077-Q1-J1-H5
 Method BLASTN
 NCBI GI g3747049
 BLAST score 67
 E value 3.0e-29
 Match length 143
 % identity 87
 NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds

Seq. No. 7107
 Contig ID 8006_1.R1040
 5'-most EST g5509188
 Method BLASTX
 NCBI GI g294845
 BLAST score 637
 E value 3.0e-66
 Match length 262
 % identity 49
 NCBI Description (L13655) membrane protein [Saccharum hybrid cultivar
 H65-7052]

Seq. No. 7108
 Contig ID 8006_2.R1040
 5'-most EST uC-gmropic058e08b1
 Method BLASTX
 NCBI GI g294845
 BLAST score 248
 E value 4.0e-21
 Match length 87
 % identity 59
 NCBI Description (L13655) membrane protein [Saccharum hybrid cultivar
 H65-7052]

Seq. No. 7109
 Contig ID 8013_1.R1040
 5'-most EST zhf700960701.h1
 Method BLASTX
 NCBI GI g2914706
 BLAST score 719

histone H3 [Onobrychis viciifolia]

Seq. No. 7125
 Contig ID 8102_1.R1040
 5'-most EST pmv700890295.h1
 Method BLASTX
 NCBI GI g3021409
 BLAST score 668
 E value 5.0e-70
 Match length 244
 % identity 25
 NCBI Description (Y12781) transducin (beta) like 1 protein [Homo sapiens]

Seq. No. 7126
 Contig ID 8111_1.R1040
 5'-most EST LIB3039-045-Q1-E1-H1

Seq. No. 7127
 Contig ID 8117_1.R1040
 5'-most EST LIB3039-045-Q1-E1-H8

Seq. No. 7128
 Contig ID 8122_1.R1040
 5'-most EST sat701014331.h1
 Method BLASTX
 NCBI GI g1871185
 BLAST score 231
 E value 8.0e-19
 Match length 115
 % identity 37
 NCBI Description (U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No. 7129
 Contig ID 8126_1.R1040
 5'-most EST LIB3039-045-Q1-E1-F6
 Method BLASTX
 NCBI GI g125722
 BLAST score 284
 E value 4.0e-25
 Match length 176
 % identity 47
 NCBI Description KUNITZ-TYPE TRYPSIN INHIBITOR KTI1 PRECURSOR
 >gi_81814_pir_JQ1091 trypsin inhibitor KTI1 (Kunitz) -
 soybean >gi_256635_bbs_115028 (S45035) Kunitz trypsin
 inhibitor KTI1 [soybeans, Peptide, 203 aa] [Glycine max]

Seq. No. 7130
 Contig ID 8127_1.R1040
 5'-most EST leu701149923.h1
 Method BLASTX
 NCBI GI g4007792
 BLAST score 246
 E value 9.0e-21
 Match length 65
 % identity 71
 NCBI Description (AL034463) Xenopus 14s cohesin smc1 subunit homolog
 [Schizosaccharomyces pombe]

Seq. No. 7131
 Contig ID 8129_1.R1040
 5'-most EST g5676949
 Method BLASTN
 NCBI GI g303838
 BLAST score 72
 E value 7.0e-32
 Match length 208
 % identity 84
 NCBI Description Rice mRNA for 40S subunit ribosomal protein, complete cds

Seq. No. 7132
 Contig ID 8129_2.R1040
 5'-most EST jC-gmf102220076f03d1

Seq. No. 7133
 Contig ID 8129_3.R1040
 5'-most EST jC-gmst02400007d04d1
 Method BLASTX
 NCBI GI g2129648
 BLAST score 160
 E value 2.0e-10
 Match length 189
 % identity 34
 NCBI Description MYB-related protein 33,3K - Arabidopsis thaliana
 >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein
 [Arabidopsis thaliana]

Seq. No. 7134
 Contig ID 8129_4.R1040
 5'-most EST LIB3040-034-Q1-E1-F5
 Method BLASTX
 NCBI GI g548852
 BLAST score 368
 E value 3.0e-35
 Match length 82
 % identity 82
 NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_481227_pir_S38357 ribosomal
 protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
 subunit ribosomal protein [Oryza sativa]

Seq. No. 7135
 Contig ID 8131_1.R1040
 5'-most EST g4405656

Seq. No. 7136
 Contig ID 8136_1.R1040
 5'-most EST ssr700557227.h1

Seq. No. 7137
 Contig ID 8136_2.R1040
 5'-most EST kl1701213934.h1

Seq. No. 7138
 Contig ID 8136_3.R1040
 5'-most EST xpa700792412.h1

Seq. No. 7139
 Contig ID 8139_1.R1040
 5'-most EST LIB3051-030-Q1-K1-D10

Seq. No. 7140
 Contig ID 8147_1.R1040
 5'-most EST rrt700645919.h1

Seq. No. 7141
 Contig ID 8150_1.R1040
 5'-most EST trc700565861.h1

Seq. No. 7142
 Contig ID 8151_1.R1040
 5'-most EST ssr700556967.h1
 Method BLASTX
 NCBI GI g3150402
 BLAST score 1329
 E value 1.0e-147
 Match length 339
 % identity 79
 NCBI Description (AC004165) putative malonyl-CoA:Acyl carrier protein transacylase [Arabidopsis thaliana]

Seq. No. 7143
 Contig ID 8151_2.R1040
 5'-most EST gsv701052805.h1
 Method BLASTX
 NCBI GI g2347187
 BLAST score 239
 E value 6.0e-20
 Match length 90
 % identity 60
 NCBI Description (AC002338) putative malonyl-CoA:Acyl carrier protein transacylase, 3' partial [Arabidopsis thaliana]

Seq. No. 7144
 Contig ID 8151_3.R1040
 5'-most EST trc700567853.h1

Seq. No. 7145
 Contig ID 8153_1.R1040
 5'-most EST LIB3087-010-Q1-K1-D4
 Method BLASTX
 NCBI GI g1350720
 BLAST score 456
 E value 2.0e-45
 Match length 111
 % identity 77
 NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 7146
 Contig ID 8154_2.R1040
 5'-most EST LIB3039-045-Q1-E1-C5

Seq. No. 7147

Contig ID	8158_1.R1040
5'-most EST	LIB3040-030-Q1-E1-E5
Method	BLASTX
NCBI GI	g122003
BLAST score	404
E value	4.0e-39
Match length	115
% identity	72
NCBI Description	HISTONE H2A >gi_82089_pir__JQ1182 histone H2A.1 - tomato
Seq. No.	7148
Contig ID	8173_1.R1040
5'-most EST	LIB3039-021-Q1-E1-H8
Method	BLASTX
NCBI GI	g2262151
BLAST score	374
E value	2.0e-35
Match length	198
% identity	46
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]
Seq. No.	7149
Contig ID	8173_2.R1040
5'-most EST	bth700846442.h1
Seq. No.	7150
Contig ID	8178_1.R1040
5'-most EST	jex700909126.h1
Seq. No.	7151
Contig ID	8189_1.R1040
5'-most EST	LIB3039-044-Q1-E1-F4
Method	BLASTX
NCBI GI	g4314388
BLAST score	475
E value	1.0e-47
Match length	129
% identity	69
NCBI Description	(AC006232) hypothetical protein [Arabidopsis thaliana]
Seq. No.	7152
Contig ID	8189_2.R1040
5'-most EST	sat701006251.h2
Method	BLASTX
NCBI GI	g4314388
BLAST score	394
E value	3.0e-38
Match length	117
% identity	64
NCBI Description	(AC006232) hypothetical protein [Arabidopsis thaliana]
Seq. No.	7153
Contig ID	8198_1.R1040
5'-most EST	LIB3039-044-Q1-E1-G6
Method	BLASTX
NCBI GI	g2281094

BLAST score 508
 E value 2.0e-51
 Match length 132
 % identity 71
 NCBI Description (AC002333) molybdenum cofactor biosynthesis protein E
 isolog [Arabidopsis thaliana] >gi_4469121_emb_CAB38428_
 (AJ133519) molybdopterin synthase large subunit
 [Arabidopsis thaliana]

Seq. No. 7154
 Contig ID 8204_1.R1040
 5'-most EST kmv700738093.h1
 Method BLASTX
 NCBI GI g2339980
 BLAST score 380
 E value 2.0e-36
 Match length 164
 % identity 55
 NCBI Description (Y11337) RGA2 protein [Arabidopsis thaliana]

Seq. No. 7155
 Contig ID 8204_2.R1040
 5'-most EST jex700904794.h1
 Method BLASTX
 NCBI GI g2339978
 BLAST score 247
 E value 5.0e-21
 Match length 100
 % identity 60
 NCBI Description (Y11336) RGA1 protein [Arabidopsis thaliana]

Seq. No. 7156
 Contig ID 8217_1.R1040
 5'-most EST LIB3039-044-Q1-E1-D10

Seq. No. 7157
 Contig ID 8223_1.R1040
 5'-most EST pmv700893311.h1
 Method BLASTX
 NCBI GI g3421123
 BLAST score 1060
 E value 1.0e-116
 Match length 227
 % identity 85
 NCBI Description (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis
 thaliana]

Seq. No. 7158
 Contig ID 8226_1.R1040
 5'-most EST epv701109794.h1
 Method BLASTX
 NCBI GI g2832686
 BLAST score 240
 E value 6.0e-20
 Match length 138
 % identity 46
 NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Contig ID 8246_1.R1040
5'-most EST LIB3040-008-Q1-E1-A8

Seq. No. 7165
Contig ID 8249_1.R1040
5'-most EST LIB3039-043-Q1-E1-G12
Method BLASTX
NCBI GI g3309170
BLAST score 269
E value 3.0e-23
Match length 130
% identity 45
NCBI Description (AF071314) COP9 complex subunit 4 [Mus musculus]

Seq. No. 7166
Contig ID 8249_2.R1040
5'-most EST LIB3109-005-Q1-K1-H3
Method BLASTX
NCBI GI g3309170
BLAST score 721
E value 4.0e-76
Match length 284
% identity 53
NCBI Description (AF071314) COP9 complex subunit 4 [Mus musculus]

Seq. No. 7167
Contig ID 8258_1.R1040
5'-most EST LIB3039-043-Q1-E1-D6
Method BLASTX
NCBI GI g4432835
BLAST score 406
E value 3.0e-39
Match length 141
% identity 52
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 7168
Contig ID 8263_1.R1040
5'-most EST zsq701127333.h1
Method BLASTX
NCBI GI g232031
BLAST score 589
E value 1.0e-60
Match length 224
% identity 54
NCBI Description ELONGATION FACTOR 1 BETA' >gi_322851_pir_S29224
translation elongation factor eEF-1 beta' chain - rice
>gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
[Oryza sativa]

Seq. No. 7169
Contig ID 8263_3.R1040
5'-most EST smc700749004.h1
Method BLASTX
NCBI GI g232031
BLAST score 273
E value 6.0e-24

Match length 76
 % identity 66
 NCBI Description ELONGATION FACTOR 1 BETA' >gi_322851_pir_S29224
 translation elongation factor eEF-1 beta' chain - rice
 >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
 [Oryza sativa]

Seq. No. 7170
 Contig ID 8263_4.R1040
 5'-most EST jC-gmro02800025g06d1
 Method BLASTN
 NCBI GI g398607
 BLAST score 35
 E value 3.0e-10
 Match length 59
 % identity 90
 NCBI Description A.thaliana mRNA for elongation factor 1 beta

Seq. No. 7171
 Contig ID 8269_1.R1040
 5'-most EST eep700867383.h1
 Method BLASTX
 NCBI GI g2559012
 BLAST score 1412
 E value 1.0e-157
 Match length 373
 % identity 73
 NCBI Description (AF026293) chaperonin containing t-complex polypeptide 1,
 beta subunit; CCT-beta [Homo sapiens] >gi_4090929
 (AF026166) chaperonin-containing TCP-1 beta subunit homolog
 [Homo sapiens]

Seq. No. 7172
 Contig ID 8278_1.R1040
 5'-most EST ncj700979022.h1
 Method BLASTX
 NCBI GI g3618214
 BLAST score 215
 E value 8.0e-17
 Match length 189
 % identity 31
 NCBI Description (AL031579) dihydrofolate reductase [Schizosaccharomyces
 pombe]

Seq. No. 7173
 Contig ID 8287_1.R1040
 5'-most EST uC-gmrominsoyl13h05b1
 Method BLASTX
 NCBI GI g2129742
 BLAST score 295
 E value 1.0e-26
 Match length 75
 % identity 73
 NCBI Description stress-induced protein OZI1 precursor - Arabidopsis
 thaliana >gi_790583 (U20347) mRNA corresponding to this
 gene accumulates in response to ozone stress and pathogen
 (bacterial) infection; putative pathogenesis-related

protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No
definition line found [Arabidopsis thaliana]

Seq. No. 7174
Contig ID 8287_2.R1040
5'-most EST gsv701050369.h1
Method BLASTX
NCBI GI g2129742
BLAST score 302
E value 2.0e-27
Match length 75
% identity 73
NCBI Description stress-induced protein OZI1 precursor - Arabidopsis
thaliana >gi_790583 (U20347) mRNA corresponding to this
gene accumulates in response to ozone stress and pathogen
(bacterial) infection; putative pathogenesis-related
protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No
definition line found [Arabidopsis thaliana]

Seq. No. 7175
Contig ID 8287_3.R1040
5'-most EST LIB3040-050-Q1-E1-F7
Method BLASTX
NCBI GI g2129742
BLAST score 295
E value 1.0e-26
Match length 75
% identity 72
NCBI Description stress-induced protein OZI1 precursor - Arabidopsis
thaliana >gi_790583 (U20347) mRNA corresponding to this
gene accumulates in response to ozone stress and pathogen
(bacterial) infection; putative pathogenesis-related
protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No
definition line found [Arabidopsis thaliana]

Seq. No. 7176
Contig ID 8287_4.R1040
5'-most EST uC-gmflminsoy035e03b1
Method BLASTX
NCBI GI g2129742
BLAST score 299
E value 3.0e-27
Match length 75
% identity 73
NCBI Description stress-induced protein OZI1 precursor - Arabidopsis
thaliana >gi_790583 (U20347) mRNA corresponding to this
gene accumulates in response to ozone stress and pathogen
(bacterial) infection; putative pathogenesis-related
protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No
definition line found [Arabidopsis thaliana]

Seq. No. 7177
Contig ID 8287_5.R1040
5'-most EST g4313658
Method BLASTX
NCBI GI g2129742
BLAST score 283

Contig ID 8294_1.R1040
 5'-most EST LIB3039-043-Q1-E1-A4
 Method BLASTX
 NCBI GI g3759184
 BLAST score 165
 E value 1.0e-11
 Match length 66
 % identity 47
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 7183
 Contig ID 8295_1.R1040
 5'-most EST leu701155106.h1
 Method BLASTX
 NCBI GI g232024
 BLAST score 163
 E value 2.0e-10
 Match length 247
 % identity 34
 NCBI Description PROTEIN E6 >gi_421806_pir_A46130 fiber protein - upland cotton >gi_2129498_pir_S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi_1000084 (U30505) E6 [Gossypium hirsutum]

Seq. No. 7184
 Contig ID 8295_2.R1040
 5'-most EST jC-gmro02910020g09a1

Seq. No. 7185
 Contig ID 8300_1.R1040
 5'-most EST LIB3039-043-Q1-E1-B2
 Method BLASTX
 NCBI GI g4097547
 BLAST score 171
 E value 8.0e-12
 Match length 77
 % identity 35
 NCBI Description (U64906) ATEP3 [Arabidopsis thaliana]

Seq. No. 7186
 Contig ID 8301_1.R1040
 5'-most EST LIB3039-043-Q1-E1-B4
 Method BLASTX
 NCBI GI g3367593
 BLAST score 312
 E value 3.0e-28
 Match length 129
 % identity 45
 NCBI Description (AL031135) putative protein [Arabidopsis thaliana] >gi_3805841_emb_CAA21461_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 7187
 Contig ID 8304_1.R1040
 5'-most EST LIB3039-042-Q1-E1-G5

Seq. No. 7188
 Contig ID 8309_1.R1040
 5'-most EST g5677411

Seq. No. 7189
 Contig ID 8318_1.R1040
 5'-most EST LIB3049-043-Q1-E1-C1
 Method BLASTX
 NCBI GI g1707074
 BLAST score 253
 E value 2.0e-21
 Match length 209
 % identity 34
 NCBI Description (U80450) M01E11.2 [Caenorhabditis elegans]

Seq. No. 7190
 Contig ID 8325_1.R1040
 5'-most EST LIB3039-021-Q1-E1-H6
 Method BLASTX
 NCBI GI g1169782
 BLAST score 437
 E value 4.0e-43
 Match length 149
 % identity 63
 NCBI Description FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis thaliana]

Seq. No. 7191
 Contig ID 8331_1.R1040
 5'-most EST jC-gmro02910029g06a1

Seq. No. 7192
 Contig ID 8331_2.R1040
 5'-most EST g5607075

Seq. No. 7193
 Contig ID 8331_3.R1040
 5'-most EST vzy700753608.h1

Seq. No. 7194
 Contig ID 8331_4.R1040
 5'-most EST LIB3039-042-Q1-E1-C7

Seq. No. 7195
 Contig ID 8340_1.R1040
 5'-most EST pmv700889160.h1
 Method BLASTX
 NCBI GI g2832642
 BLAST score 407
 E value 5.0e-39
 Match length 463
 % identity 29
 NCBI Description (AL021710) putative protein [Arabidopsis thaliana]

Seq. No. 7196
 Contig ID 8344_1.R1040
 5'-most EST LIB3107-031-Q1-K1-C4

Method BLASTX
 NCBI GI g2982283
 BLAST score 382
 E value 2.0e-36
 Match length 148
 % identity 51
 NCBI Description (AF051226) PREG-like protein [Picea mariana]

Seq. No. 7197
 Contig ID 8344_2.R1040
 5'-most EST LIB3107-072-Q1-K1-C8

Seq. No. 7198
 Contig ID 8349_1.R1040
 5'-most EST LIB3170-011-Q1-J1-E1
 Method BLASTX
 NCBI GI g459009
 BLAST score 236
 E value 1.0e-19
 Match length 79
 % identity 54
 NCBI Description (U00037) similar to multifunctional aminoacyl-tRNA synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans]

Seq. No. 7199
 Contig ID 8349_2.R1040
 5'-most EST LIB3072-025-Q1-E1-A6
 Method BLASTX
 NCBI GI g459009
 BLAST score 211
 E value 8.0e-17
 Match length 80
 % identity 49
 NCBI Description (U00037) similar to multifunctional aminoacyl-tRNA synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans]

Seq. No. 7200
 Contig ID 8349_3.R1040
 5'-most EST taw700657102.h1

Seq. No. 7201
 Contig ID 8353_1.R1040
 5'-most EST asn701131479.h1
 Method BLASTX
 NCBI GI g2911060
 BLAST score 154
 E value 5.0e-10
 Match length 88
 % identity 29
 NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
 >gi_3297826_emb_CAA19884.1_ (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 7202
 Contig ID 8361_1.R1040

5'-most EST LIB3039-041-Q1-E1-F12

Seq. No. 7203
 Contig ID 8370 1.R1040
 5'-most EST ncj700981540.h1
 Method BLASTX
 NCBI GI g3335337
 BLAST score 446
 E value 5.0e-44
 Match length 119
 % identity 76
 NCBI Description (AC004512) Similar to acyl carrier protein, mitochondrial precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330 come from this gene

Seq. No. 7204
 Contig ID 8370 2.R1040
 5'-most EST LIB3039-033-Q1-E1-E11
 Method BLASTX
 NCBI GI g3335337
 BLAST score 327
 E value 2.0e-30
 Match length 115
 % identity 65
 NCBI Description (AC004512) Similar to acyl carrier protein, mitochondrial precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330 come from this gene

Seq. No. 7205
 Contig ID 8376 1.R1040
 5'-most EST LIB3049-018-Q1-E1-D1
 Method BLASTX
 NCBI GI g3135265
 BLAST score 354
 E value 3.0e-33
 Match length 101
 % identity 68
 NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 7206
 Contig ID 8376 2.R1040
 5'-most EST LIB3109-034-Q1-K1-B11
 Method BLASTX
 NCBI GI g3135265
 BLAST score 441
 E value 1.0e-43
 Match length 101
 % identity 81
 NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 7207
 Contig ID 8378 1.R1040
 5'-most EST LIB3109-006-Q1-K1-B12

NCBI GI g2586127
BLAST score 309
E value 4.0e-28
Match length 124
% identity 52
NCBI Description (U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No. 7214
Contig ID 8408_2.R1040
5'-most EST uxk700668489.h1

Seq. No. 7215
Contig ID 8409_1.R1040
5'-most EST smw700646216.h1

Seq. No. 7216
Contig ID 8413_1.R1040
5'-most EST jC-gmle01810041a04a1

Seq. No. 7217
Contig ID 8413_2.R1040
5'-most EST LIB3039-018-Q1-E1-H4

Seq. No. 7218
Contig ID 8417_1.R1040
5'-most EST LIB3074-029-Q1-K1-A6
Method BLASTX
NCBI GI g1173456
BLAST score 328
E value 3.0e-30
Match length 97
% identity 58
NCBI Description SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]

Seq. No. 7219
Contig ID 8417_2.R1040
5'-most EST LIB3170-062-Q1-J1-A1
Method BLASTX
NCBI GI g2708715
BLAST score 142
E value 1.0e-08
Match length 46
% identity 54
NCBI Description (AF038598) small nuclear ribonucleoprotein Sm D3 [Drosophila melanogaster]

Seq. No. 7220
Contig ID 8422_1.R1040
5'-most EST trc700562809.h1
Method BLASTX
NCBI GI g1877026
BLAST score 202
E value 1.0e-20
Match length 86
% identity 55
NCBI Description (D78336) ribosomal protein S19 [Oryza sativa]

Seq. No. 7221
 Contig ID 8427_1.R1040
 5'-most EST LIB3094-078-Q1-K1-A11
 Method BLASTX
 NCBI GI g4508069
 BLAST score 230
 E value 7.0e-19
 Match length 161
 % identity 35
 NCBI Description (AC005882) 12246 [Arabidopsis thaliana]

Seq. No. 7222
 Contig ID 8429_1.R1040
 5'-most EST leu701145719.h1
 Method BLASTX
 NCBI GI g730456
 BLAST score 615
 E value 7.0e-64
 Match length 140
 % identity 80
 NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 7223
 Contig ID 8438_1.R1040
 5'-most EST wvk700681268.h1
 Method BLASTX
 NCBI GI g2493694
 BLAST score 299
 E value 6.0e-27
 Match length 119
 % identity 53
 NCBI Description PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII 6.1 KD PROTEIN) >gi_1076268_pir_S53025 photosystem II protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein of photosystem II [Spinacia oleracea]

Seq. No. 7224
 Contig ID 8438_2.R1040
 5'-most EST leu701147974.h1

Seq. No. 7225
 Contig ID 8438_3.R1040
 5'-most EST LIB3073-017-Q1-K1-G7
 Method BLASTX
 NCBI GI g2493694
 BLAST score 214
 E value 4.0e-17
 Match length 116
 % identity 40
 NCBI Description PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII 6.1 KD PROTEIN) >gi_1076268_pir_S53025 photosystem II protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein of photosystem II [Spinacia oleracea]

Seq. No. 7226
 Contig ID 8441_1.R1040

5'-most EST vwf700675988.h1

Seq. No. 7227
 Contig ID 8446_1.R1040
 5'-most EST fC-gmro700866877d3
 Method BLASTX
 NCBI GI g1169533
 BLAST score 155
 E value 3.0e-10
 Match length 37
 % identity 86
 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
 >gi_515827_emb_CAA56645_ (X80474) enolase [Neocallimastix
 frontalis]

Seq. No. 7228
 Contig ID 8464_1.R1040
 5'-most EST LIB3049-034-Q1-E1-E11
 Method BLASTN
 NCBI GI g3927915
 BLAST score 135
 E value 1.0e-69
 Match length 311
 % identity 86
 NCBI Description Fagus sylvatica mRNA for glycine-rich protein

Seq. No. 7229
 Contig ID 8464_2.R1040
 5'-most EST uaw700663386.h1
 Method BLASTX
 NCBI GI g1076626
 BLAST score 498
 E value 2.0e-50
 Match length 92
 % identity 98
 NCBI Description glycine rich protein - common tobacco
 >gi_790473_emb_CAA58702_ (X83731) soluble, glycine rich
 protein [Nicotiana tabacum]

Seq. No. 7230
 Contig ID 8464_3.R1040
 5'-most EST zpv700760105.h1
 Method BLASTX
 NCBI GI g1076626
 BLAST score 166
 E value 5.0e-16
 Match length 46
 % identity 96
 NCBI Description glycine rich protein - common tobacco
 >gi_790473_emb_CAA58702_ (X83731) soluble, glycine rich
 protein [Nicotiana tabacum]

Seq. No. 7231
 Contig ID 8464_4.R1040
 5'-most EST awf700836556.h1
 Method BLASTN

NCBI GI g3927915
 BLAST score 61
 E value 7.0e-26
 Match length 133
 % identity 86
 NCBI Description Fagus sylvatica mRNA for glycine-rich protein

Seq. No. 7232
 Contig ID 8465 1.R1040
 5'-most EST LIB3039-039-Q1-E1-G9
 Method BLASTN
 NCBI GI g3819163
 BLAST score 283
 E value 1.0e-158
 Match length 335
 % identity 96
 NCBI Description Glycine max cctd gene

Seq. No. 7233
 Contig ID 8465 2.R1040
 5'-most EST zhF700956825.h1
 Method BLASTN
 NCBI GI g3819163
 BLAST score 146
 E value 2.0e-76
 Match length 319
 % identity 93
 NCBI Description Glycine max cctd gene

Seq. No. 7234
 Contig ID 8468 1.R1040
 5'-most EST uC-gmropic023h03b1
 Method BLASTX
 NCBI GI g3935167
 BLAST score 533
 E value 3.0e-54
 Match length 123
 % identity 84
 NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]

Seq. No. 7235
 Contig ID 8468 2.R1040
 5'-most EST wrG700787076.h2
 Method BLASTX
 NCBI GI g3935167
 BLAST score 520
 E value 7.0e-53
 Match length 123
 % identity 83
 NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]

Seq. No. 7236
 Contig ID 8473 1.R1040
 5'-most EST bth700845213.h1
 Method BLASTX
 NCBI GI g2979550
 BLAST score 437

Seq. No. 7242
 Contig ID 8476_5.R1040
 5'-most EST uaw700666680.h1
 Method BLASTX
 NCBI GI g4056503
 BLAST score 180
 E value 3.0e-13
 Match length 36
 % identity 92
 NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 7243
 Contig ID 8476_8.R1040
 5'-most EST gsv701054710.h1

Seq. No. 7244
 Contig ID 8476_11.R1040
 5'-most EST hyd700727629.h1
 Method BLASTX
 NCBI GI g4056488
 BLAST score 187
 E value 1.0e-28
 Match length 96
 % identity 65
 NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 7245
 Contig ID 8483_1.R1040
 5'-most EST LIB3051-051-Q1-K1-F9

Seq. No. 7246
 Contig ID 8483_2.R1040
 5'-most EST awf700842960.h1

Seq. No. 7247
 Contig ID 8483_3.R1040
 5'-most EST uC-gmrominsoy204g02b1

Seq. No. 7248
 Contig ID 8487_1.R1040
 5'-most EST LIB3039-039-Q1-E1-G5
 Method BLASTX
 NCBI GI g2809246
 BLAST score 246
 E value 5.0e-21
 Match length 78
 % identity 62
 NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]

Seq. No. 7249
 Contig ID 8490_1.R1040
 5'-most EST LIB3039-039-Q1-E1-F2
 Method BLASTX
 NCBI GI g1065515
 BLAST score 359
 E value 5.0e-34

0001016 9104360

Match length 154
 % identity 47
 NCBI Description (U40420) weak similarity to procollagen alpha chain 1(V)
 chain [Caenorhabditis elegans]

Seq. No. 7250
 Contig ID 8492_1.R1040
 5'-most EST leu701144444.h1
 Method BLASTX
 NCBI GI g2351374
 BLAST score 533
 E value 2.0e-54
 Match length 111
 % identity 92
 NCBI Description (U54560) putative 26S proteasome subunit athMOV34
 [Arabidopsis thaliana]

Seq. No. 7251
 Contig ID 8493_1.R1040
 5'-most EST leu701149723.h1
 Method BLASTX
 NCBI GI g3810594
 BLAST score 456
 E value 2.0e-45
 Match length 123
 % identity 74
 NCBI Description (AC005398) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7252
 Contig ID 8494_1.R1040
 5'-most EST LIB3039-039-Q1-E1-E4
 Method BLASTX
 NCBI GI g2702274
 BLAST score 362
 E value 2.0e-34
 Match length 103
 % identity 67
 NCBI Description (AC003033) unknown protein [Arabidopsis thaliana]

Seq. No. 7253
 Contig ID 8497_1.R1040
 5'-most EST LIB3039-039-Q1-E1-F1
 Method BLASTX
 NCBI GI g2894596
 BLAST score 639
 E value 1.0e-66
 Match length 187
 % identity 67
 NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 7254
 Contig ID 8497_2.R1040
 5'-most EST trc700562114.h1

Seq. No. 7255
 Contig ID 8500_1.R1040
 5'-most EST LIB3051-018-Q1-E1-H7

5'-most EST	LIB3074-024-Q1-E1-C12
Seq. No.	7267
Contig ID	8552_1.R1040
5'-most EST	LIB3039-038-Q1-E1-D7
Seq. No.	7268
Contig ID	8558_1.R1040
5'-most EST	LIB3039-038-Q1-E1-C7
Seq. No.	7269
Contig ID	8562_1.R1040
5'-most EST	LIB3094-046-Q1-K1-H11
Method	BLASTN
NCBI GI	g499066
BLAST score	488
E value	0.0e+00
Match length	678
% identity	99
NCBI Description	G.max gmrl gene
Seq. No.	7270
Contig ID	8565_1.R1040
5'-most EST	jC-gmro02910006c04a1
Seq. No.	7271
Contig ID	8565_2.R1040
5'-most EST	gsv701048378.h1
Seq. No.	7272
Contig ID	8570_1.R1040
5'-most EST	taw700655350.h1
Seq. No.	7273
Contig ID	8579_1.R1040
5'-most EST	jC-gmst02400075g11d1
Method	BLASTX
NCBI GI	g2367418
BLAST score	489
E value	3.0e-49
Match length	140
% identity	62
NCBI Description	(AF000392) peptide tr
Seq. No.	7274
Contig ID	8581_1.R1040
5'-most EST	LIB3039-037-Q1-E1-G7
Seq. No.	7275
Contig ID	8584_1.R1040
5'-most EST	gsv701050179.h1
Seq. No.	7276
Contig ID	8591_1.R1040
5'-most EST	V4L-01-Q1-B1-C3
Method	BLASTX
NCBI GI	g3451075

BLAST score 1683
 E value 0.0e+00
 Match length 432
 % identity 70
 NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 7277
 Contig ID 8594_1.R1040
 5'-most EST LIB3039-012-Q1-E1-D9
 Method BLASTX
 NCBI GI g2851506
 BLAST score 323
 E value 5.0e-30
 Match length 82
 % identity 70
 NCBI Description DYSKERIN (NUCLEOLAR PROTEIN NAP57)
 >gi_2739325_emb_CAA84402_ (Z34922) NAP57 [Rattus norvegicus]

Seq. No. 7278
 Contig ID 8594_2.R1040
 5'-most EST LIB3051-034-Q1-K1-G7
 Method BLASTX
 NCBI GI g2851506
 BLAST score 340
 E value 5.0e-34
 Match length 98
 % identity 71
 NCBI Description DYSKERIN (NUCLEOLAR PROTEIN NAP57)
 >gi_2739325_emb_CAA84402_ (Z34922) NAP57 [Rattus norvegicus]

Seq. No. 7279
 Contig ID 8617_1.R1040
 5'-most EST kl1701208274.h1

Seq. No. 7280
 Contig ID 8618_1.R1040
 5'-most EST LIB3049-024-Q1-E1-D10
 Method BLASTX
 NCBI GI g3176874
 BLAST score 2036
 E value 0.0e+00
 Match length 733
 % identity 71
 NCBI Description (AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No. 7281
 Contig ID 8618_5.R1040
 5'-most EST ncj700978984.h1
 Method BLASTX
 NCBI GI g3176874
 BLAST score 225
 E value 1.0e-18
 Match length 62
 % identity 61

E value	7.0e-83
Match length	285
% identity	58
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]
Seq. No.	7303
Contig ID	8685_3.R1040
5'-most EST	LIB3051-013-Q1-E1-F6
Seq. No.	7304
Contig ID	8691_1.R1040
5'-most EST	LIB3072-014-Q1-E1-D8
Seq. No.	7305
Contig ID	8699_1.R1040
5'-most EST	LIB3039-035-Q1-E1-E2
Method	BLASTX
NCBI GI	g2827086
BLAST score	322
E value	6.0e-30
Match length	100
% identity	58
NCBI Description	(AF022778) DNA recombination and repair protein [Homo sapiens] >gi_3328152 (AF073362) endo/exonuclease Mre11 [Homo sapiens]
Seq. No.	7306
Contig ID	8701_1.R1040
5'-most EST	LIB3039-005-Q1-E1-B3
Seq. No.	7307
Contig ID	8702_1.R1040
5'-most EST	LIB3039-035-Q1-E1-E5
Method	BLASTX
NCBI GI	g4335759
BLAST score	165
E value	2.0e-11
Match length	98
% identity	47
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.	7308
Contig ID	8706_1.R1040
5'-most EST	leu701155875.h1
Seq. No.	7309
Contig ID	8707_1.R1040
5'-most EST	LIB3039-035-Q1-E1-C12
Method	BLASTX
NCBI GI	g2832629
BLAST score	153
E value	7.0e-10
Match length	116
% identity	30
NCBI Description	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No. 7310
Contig ID 8709_1.R1040
5'-most EST gsv701047702.h1

Seq. No. 7311
Contig ID 8714_1.R1040
5'-most EST kl1701211410.h1
Method BLASTX
NCBI GI g1076427
BLAST score 570
E value 6.0e-59
Match length 115
% identity 89
NCBI Description ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis thaliana

Seq. No. 7312
Contig ID 8716_1.R1040
5'-most EST LIB3049-055-Q1-E1-H4
Method BLASTN
NCBI GI g3860314
BLAST score 207
E value 1.0e-112
Match length 345
% identity 92
NCBI Description Cicer arietinum mRNA for 40S ribosomal protein S19, partial

Seq. No. 7313
Contig ID 8716_2.R1040
5'-most EST LIB3051-032-Q1-K1-G5
Method BLASTN
NCBI GI g3860314
BLAST score 123
E value 1.0e-62
Match length 275
% identity 86
NCBI Description Cicer arietinum mRNA for 40S ribosomal protein S19, partial

Seq. No. 7314
Contig ID 8717_1.R1040
5'-most EST LIB3106-019-Q1-K1-C1

Seq. No. 7315
Contig ID 8720_1.R1040
5'-most EST LIB3039-035-Q1-E1-A9
Method BLASTX
NCBI GI g2281092
BLAST score 233
E value 3.0e-19
Match length 68
% identity 72
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7316
Contig ID 8721_1.R1040
5'-most EST zhf700958240.h1

BLAST score 243
 E value 9.0e-21
 Match length 77
 % identity 58
 NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No. 7332
 Contig ID 8754_1.R1040
 5'-most EST LIB3039-034-Q1-E1-E7

Seq. No. 7333
 Contig ID 8759_1.R1040
 5'-most EST leu701153853.h1

Seq. No. 7334
 Contig ID 8764_1.R1040
 5'-most EST LIB3039-016-Q1-E1-C8
 Method BLASTN
 NCBI GI g3281847
 BLAST score 42
 E value 2.0e-14
 Match length 86
 % identity 87
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)

Seq. No. 7335
 Contig ID 8764_2.R1040
 5'-most EST fua701040759.h1
 Method BLASTN
 NCBI GI g3281847
 BLAST score 42
 E value 2.0e-14
 Match length 86
 % identity 87
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)

Seq. No. 7336
 Contig ID 8765_1.R1040
 5'-most EST leu701149120.h1
 Method BLASTX
 NCBI GI g2739279
 BLAST score 535
 E value 2.0e-54
 Match length 208
 % identity 53
 NCBI Description (AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi_2791348_emb_CAA11154_ (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

Seq. No. 7337
 Contig ID 8767_1.R1040
 5'-most EST zsg701124165.h1

Seq. No. 7338
 Contig ID 8777_1.R1040

5'-most EST LIB3039-034-Q1-E1-B2
 Method BLASTX
 NCBI GI g3845099
 BLAST score 169
 E value 1.0e-11
 Match length 124
 % identity 3
 NCBI Description (AE001373) predicted secreted protein [Plasmodium falciparum]

Seq. No. 7339
 Contig ID 8777_2.R1040
 5'-most EST LIB3049-022-Q1-E1-D4

Seq. No. 7340
 Contig ID 8777_4.R1040
 5'-most EST LIB3073-004-Q1-K1-A6

Seq. No. 7341
 Contig ID 8780_1.R1040
 5'-most EST LIB3051-082-Q1-K1-D2
 Method BLASTN
 NCBI GI g2696018
 BLAST score 108
 E value 1.0e-53
 Match length 332
 % identity 83
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No. 7342
 Contig ID 8783_1.R1040
 5'-most EST epX701106758.h1

Seq. No. 7343
 Contig ID 8784_1.R1040
 5'-most EST zhF700961867.h1
 Method BLASTX
 NCBI GI g3023956
 BLAST score 191
 E value 3.0e-14
 Match length 168
 % identity 4
 NCBI Description VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 >gi_607003 (L28125) beta transducin-like protein [Podospora anserina]

Seq. No. 7344
 Contig ID 8792_1.R1040
 5'-most EST LIB3039-033-Q1-E1-G5
 Method BLASTX
 NCBI GI g1181589
 BLAST score 284
 E value 2.0e-25
 Match length 120
 % identity 54
 NCBI Description (D83070) high mobility group protein [Canavalia gladiata] >gi_1483173_dbj_BAA13133_ (D86594) high mobility group

[illegible]

Seq. No.	7351
Contig ID	8815_3.R1040
5'-most EST	LIB3049-017-Q1-E1-H7

00001016-101000

Method BLASTN
NCBI GI g432488
BLAST score 135
E value 2.0e-69
Match length 282
% identity 87
NCBI Description Wheat initiation factor 1A (eIF-1A) mRNA

Seq. No. 7352
Contig ID 8815_4.R1040
5'-most EST LIB3051-053-Q1-K2-H1
Method BLASTN
NCBI GI g432488
BLAST score 137
E value 5.0e-71
Match length 217
% identity 91
NCBI Description Wheat initiation factor 1A (eIF-1A) mRNA

Seq. No. 7353
Contig ID 8815_6.R1040
5'-most EST zsg701118418.h1
Method BLASTN
NCBI GI g432488
BLAST score 50
E value 3.0e-19
Match length 74
% identity 92
NCBI Description Wheat initiation factor 1A (eIF-1A) mRNA

Seq. No. 7354
Contig ID 8821_1.R1040
5'-most EST LIB3039-033-Q1-E1-B7
Method BLASTX
NCBI GI g4539005
BLAST score 295
E value 1.0e-26
Match length 132
% identity 46
NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 7355
Contig ID 8825_1.R1040
5'-most EST fua701040082.h1
Method BLASTX
NCBI GI g1345933
BLAST score 1398
E value 1.0e-155
Match length 296
% identity 89
NCBI Description CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS)
>gi_1084323_pir_S53007 citrate synthase - cucurbit
>gi_975633_dbj_BAA07328_(D38132) glyoxysomal citrate
synthase [Cucurbita sp.]

Seq. No. 7356
Contig ID 8828_1.R1040

Seq. No. 7361
 Contig ID 8842 1.R1040
 5'-most EST LIB3049-012-Q1-E1-H3
 Method BLASTX
 NCBI GI g4432837
 BLAST score 268
 E value 3.0e-23
 Match length 148
 % identity 47
 NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7362
 Contig ID 8856 1.R1040
 5'-most EST hyd700726103.h1
 Method BLASTX
 NCBI GI g3928150
 BLAST score 491
 E value 2.0e-49
 Match length 113
 % identity 83
 NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 7363
 Contig ID 8866 1.R1040
 5'-most EST LIB3039-032-Q1-E1-D9
 Method BLASTX
 NCBI GI g478318
 BLAST score 174
 E value 3.0e-12
 Match length 100
 % identity 36
 NCBI Description immunophilin p59 - mouse >gi_410499_emb_CAA50231_ (X70887)
 p59 immunophilin [Mus musculus]

Seq. No. 7364
 Contig ID 8871 1.R1040
 5'-most EST LIB3039-032-Q1-E1-E7

Seq. No. 7365
 Contig ID 8873 1.R1040
 5'-most EST leu701148713.h1
 Method BLASTX
 NCBI GI g2842486
 BLAST score 390
 E value 1.0e-37
 Match length 120
 % identity 64
 NCBI Description (AL021749) putative protein [Arabidopsis thaliana]

Seq. No. 7366
 Contig ID 8873 2.R1040
 5'-most EST LIB3039-032-Q1-E1-F1
 Method BLASTX
 NCBI GI g4204306
 BLAST score 296
 E value 6.0e-27
 Match length 88

% identity 72
NCBI Description (AC003027) lcl_prt_seq No definition line found
[Arabidopsis thaliana]

Seq. No. 7367
Contig ID 8875_1.R1040
5'-most EST LIB3039-032-Q1-E1-C2
Method BLASTX
NCBI GI g2921209
BLAST score 499
E value 2.0e-50
Match length 143
% identity 73
NCBI Description (AF026148) beta-ketoacyl-ACP synthase I [Perilla
frutescens]

Seq. No. 7368
Contig ID 8883_1.R1040
5'-most EST LIB3109-001-Q1-K1-G11
Method BLASTX
NCBI GI g2827536
BLAST score 338
E value 5.0e-31
Match length 176
% identity 41
NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7369
Contig ID 8883_3.R1040
5'-most EST LIB3107-006-Q1-K1-A7

Seq. No. 7370
Contig ID 8883_4.R1040
5'-most EST LIB3052-016-Q1-N1-E3

Seq. No. 7371
Contig ID 8891_1.R1040
5'-most EST leu701157334.h1

Seq. No. 7372
Contig ID 8892_1.R1040
5'-most EST gsv701052888.h1
Method BLASTX
NCBI GI g3881780
BLAST score 176
E value 3.0e-12
Match length 116
% identity 37
NCBI Description (Z48638) similar to lipid transfer protein [Caenorhabditis
elegans]

Seq. No. 7373
Contig ID 8901_1.R1040
5'-most EST LIB3039-004-Q1-E1-G1
Method BLASTX
NCBI GI g1183961
BLAST score 477

Method BLASTX
 NCBI GI g2827655
 BLAST score 175
 E value 5.0e-12
 Match length 208
 % identity 33
 NCBI Description (AL021637) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7385
 Contig ID 8958_1.R1040
 5'-most EST epx701109691.h1
 Method BLASTX
 NCBI GI g3204129
 BLAST score 502
 E value 1.0e-50
 Match length 133
 % identity 77
 NCBI Description (AJ006768) histone H2A [Cicer arietinum]

Seq. No. 7386
 Contig ID 8958_2.R1040
 5'-most EST LIB3074-040-Q1-K1-B2
 Method BLASTX
 NCBI GI g3776566
 BLAST score 398
 E value 1.0e-38
 Match length 106
 % identity 75
 NCBI Description (AC005388) Strong similarity to histone H2A gb_AJ006768 from Cicer arietinum. [Arabidopsis thaliana]

Seq. No. 7387
 Contig ID 8978_1.R1040
 5'-most EST LIB3039-030-Q1-E1-E7
 Method BLASTX
 NCBI GI g140474
 BLAST score 251
 E value 7.0e-21
 Match length 203
 % identity 31
 NCBI Description HYPOTHETICAL 69.2 KD PROTEIN IN HSP30-PMP1 INTERGENIC REGION >gi_83212_pir_S19434 probable transport protein YCR023c - yeast (Saccharomyces cerevisiae)
 >gi_1907167_emb_CAA42315_ (X59720) YCR023c, len:611 [Saccharomyces cerevisiae]

Seq. No. 7388
 Contig ID 8978_2.R1040
 5'-most EST leu701153306.h1
 Method BLASTX
 NCBI GI g140474
 BLAST score 159
 E value 1.0e-10
 Match length 67
 % identity 45
 NCBI Description HYPOTHETICAL 69.2 KD PROTEIN IN HSP30-PMP1 INTERGENIC REGION >gi_83212_pir_S19434 probable transport protein

Match length 102
 % identity 54
 NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No. 7411
 Contig ID 9050_1.R1040
 5'-most EST yuv700862829.h1
 Method BLASTN
 NCBI GI g536891
 BLAST score 107
 E value 9.0e-53
 Match length 264
 % identity 88
 NCBI Description Wheat mRNA for protein H2A, complete cds, clone wch2A-4

Seq. No. 7412
 Contig ID 9050_2.R1040
 5'-most EST leu701144726.h1
 Method BLASTN
 NCBI GI g536891
 BLAST score 94
 E value 4.0e-45
 Match length 274
 % identity 86
 NCBI Description Wheat mRNA for protein H2A, complete cds, clone wch2A-4

Seq. No. 7413
 Contig ID 9050_3.R1040
 5'-most EST LIB3040-021-Q1-E1-C2
 Method BLASTN
 NCBI GI g536891
 BLAST score 99
 E value 4.0e-48
 Match length 285
 % identity 86
 NCBI Description Wheat mRNA for protein H2A, complete cds, clone wch2A-4

Seq. No. 7414
 Contig ID 9050_4.R1040
 5'-most EST jC-gmle01810087g06a1
 Method BLASTX
 NCBI GI g3269284
 BLAST score 281
 E value 7.0e-25
 Match length 56
 % identity 100
 NCBI Description (AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No. 7415
 Contig ID 9053_1.R1040
 5'-most EST LIB3039-029-Q1-E1-B5

Seq. No. 7416
 Contig ID 9065_1.R1040
 5'-most EST uC-gmropic040f08b1
 Method BLASTN

NCBI GI g556421
 BLAST score 56
 E value 2.0e-22
 Match length 120
 % identity 96
 NCBI Description Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1)
 mRNA, complete cds

Seq. No. 7417
 Contig ID 9065_2.R1040
 5'-most EST gsv701051084.h1
 Method BLASTN
 NCBI GI g556421
 BLAST score 52
 E value 3.0e-20
 Match length 109
 % identity 94
 NCBI Description Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1)
 mRNA, complete cds

Seq. No. 7418
 Contig ID 9071_1.R1040
 5'-most EST pmv700894565.h1

Seq. No. 7419
 Contig ID 9076_1.R1040
 5'-most EST LIB3106-011-Q1-K1-B5
 Method BLASTX
 NCBI GI g3738329
 BLAST score 322
 E value 1.0e-29
 Match length 88
 % identity 78
 NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 7420
 Contig ID 9076_2.R1040
 5'-most EST ssr700557608.h1

Seq. No. 7421
 Contig ID 9079_1.R1040
 5'-most EST LIB3039-028-Q1-E1-H10
 Method BLASTX
 NCBI GI g4006872
 BLAST score 231
 E value 4.0e-19
 Match length 60
 % identity 73
 NCBI Description (Z99707) methionyl aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. 7422
 Contig ID 9080_1.R1040
 5'-most EST bth700845178.h1
 Method BLASTX
 NCBI GI g2708750
 BLAST score 361

Seq. No. 7441
 Contig ID 9148 1.R1040
 5'-most EST LIB3039-027-Q1-E1-H3
 Method BLASTX
 NCBI GI g2583134
 BLAST score 143
 E value 6.0e-09
 Match length 94
 % identity 46
 NCBI Description (AC002387) putative proline-rich protein [Arabidopsis thaliana]

Seq. No. 7442
 Contig ID 9154 1.R1040
 5'-most EST LIB3040-035-Q1-E1-D7

Seq. No. 7443
 Contig ID 9154 2.R1040
 5'-most EST LIB3107-050-Q1-K1-C1
 Method BLASTN
 NCBI GI g940287
 BLAST score 35
 E value 4.0e-10
 Match length 75
 % identity 87
 NCBI Description Pisum sativum L. (clone na-481-5) mRNA, complete cds

Seq. No. 7444
 Contig ID 9155 1.R1040
 5'-most EST LIB3039-027-Q1-E1-F6
 Method BLASTX
 NCBI GI g3021598
 BLAST score 171
 E value 2.0e-11
 Match length 346
 % identity 25
 NCBI Description (Y10389) nuclear protein [Xenopus laevis]

Seq. No. 7445
 Contig ID 9155 2.R1040
 5'-most EST leu701151007.h1

Seq. No. 7446
 Contig ID 9159 1.R1040
 5'-most EST LIB3087-007-Q1-K1-D5

Seq. No. 7447
 Contig ID 9169 1.R1040
 5'-most EST LIB3039-027-Q1-E1-E11

Seq. No. 7448
 Contig ID 9171 1.R1040
 5'-most EST LIB3039-027-Q1-E1-E5
 Method BLASTX
 NCBI GI g3763934
 BLAST score 226

5'-most EST g5688377
 Method BLASTX
 NCBI GI g3879734
 BLAST score 258
 E value 8.0e-22
 Match length 228
 % identity 33
 NCBI Description (Z93388) predicted using Genefinder; cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST EMBL:D74229 comes from this gene; cDNA EST EMBL:D727

Seq. No. 7458
 Contig ID 9213_1.R1040
 5'-most EST g5606317
 Method BLASTX
 NCBI GI g4220482
 BLAST score 423
 E value 2.0e-41
 Match length 135
 % identity 37
 NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7459
 Contig ID 9213_2.R1040
 5'-most EST LIB3039-026-Q1-E1-A1
 Method BLASTX
 NCBI GI g4220482
 BLAST score 226
 E value 1.0e-18
 Match length 74
 % identity 59
 NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7460
 Contig ID 9214_1.R1040
 5'-most EST LIB3039-026-Q1-E1-F5
 Method BLASTX
 NCBI GI g498040
 BLAST score 555
 E value 8.0e-57
 Match length 191
 % identity 60
 NCBI Description (L33793) ORF [Senecio odorus]

Seq. No. 7461
 Contig ID 9214_2.R1040
 5'-most EST uC-gmropic102f04b1
 Method BLASTX
 NCBI GI g498040
 BLAST score 254
 E value 6.0e-22
 Match length 70
 % identity 73
 NCBI Description (L33793) ORF [Senecio odorus]

Seq. No. 7462

>gi_1363796_pir_S59308 probable membrane protein YMR315w -
 yeast (*Saccharomyces cerevisiae*) >gi_984688_emb_CAA90833_
 (Z54141) unknown [*Saccharomyces cerevisiae*]

Seq. No. 7514
 Contig ID 9483_2.R1040
 5'-most EST uC-gmropic067b04b1

Seq. No. 7515
 Contig ID 9487_1.R1040
 5'-most EST leu701145178.h1
 Method BLASTX
 NCBI GI g4115949
 BLAST score 248
 E value 3.0e-21
 Match length 104
 % identity 55
 NCBI Description (AF118223) contains similarity to adenosine deaminases
 [*Arabidopsis thaliana*]

Seq. No. 7516
 Contig ID 9494_1.R1040
 5'-most EST uxk700672041.h1
 Method BLASTX
 NCBI GI g1170504
 BLAST score 1801
 E value 0.0e+00
 Match length 606
 % identity 61
 NCBI Description EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P82
 (IEIF-(ISO)4F P82) >gi_452440 (M95747) initiation factor
 (iso)4f p82 subunit [*Triticum aestivum*]

Seq. No. 7517
 Contig ID 9495_1.R1040
 5'-most EST pcp700991891.h1

Seq. No. 7518
 Contig ID 9511_1.R1040
 5'-most EST LIB3074-004-Q1-K1-F12
 Method BLASTX
 NCBI GI g3724328
 BLAST score 145
 E value 1.0e-08
 Match length 151
 % identity 25
 NCBI Description (AB013095) heme-binding protein [*Mus musculus*]

Seq. No. 7519
 Contig ID 9511_2.R1040
 5'-most EST LIB3109-003-Q1-K1-A6

Seq. No. 7520
 Contig ID 9522_1.R1040
 5'-most EST pcp700993234.h1
 Method BLASTX
 NCBI GI g4314356

09684016.101000

Seq. No. 7526
 Contig ID 9547_2.R1040
 5'-most EST LIB3106-067-P1-K1-F7
 Method BLASTX
 NCBI GI g2982432
 BLAST score 325
 E value 4.0e-30
 Match length 73
 % identity 81
 NCBI Description (AL022224) putative protein [Arabidopsis thaliana]

Seq. No. 7527
 Contig ID 9548_1.R1040
 5'-most EST leu701154367.h1
 Method BLASTX
 NCBI GI g4544436
 BLAST score 293
 E value 2.0e-26
 Match length 102
 % identity 60
 NCBI Description (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase, 3' partial [Arabidopsis thaliana]

Seq. No. 7528
 Contig ID 9552_1.R1040
 5'-most EST kmv700740207.h1
 Method BLASTX
 NCBI GI g2632106
 BLAST score 711
 E value 3.0e-75
 Match length 212
 % identity 61
 NCBI Description (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 7529
 Contig ID 9558_1.R1040
 5'-most EST LIB3039-019-Q1-E1-G11

Seq. No. 7530
 Contig ID 9558_2.R1040
 5'-most EST jC-gmf102220075f08a1

Seq. No. 7531
 Contig ID 9560_1.R1040
 5'-most EST vzy700754495.h1

Seq. No. 7532
 Contig ID 9562_1.R1040
 5'-most EST leu701157074.h1

Seq. No. 7533
 Contig ID 9565_1.R1040
 5'-most EST LIB3170-026-Q1-K1-C10
 Method BLASTX
 NCBI GI g3876465
 BLAST score 329

% identity	59
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	7540
Contig ID	9600_1.R1040
5'-most EST	leu701150153.h1
Method	BLASTX
NCBI GI	g549577
BLAST score	227
E value	1.0e-18
Match length	66
% identity	65
NCBI Description	HYPOTHETICAL 17.1 KD PROTEIN IN MECB-GLTX INTERGENIC REGION >gi_2127059_pir_S66120 hypothetical protein - Bacillus subtilis >gi_289281 (L14580) unknown [Bacillus subtilis] >gi_467479_dbj_BAA05325 (D26185) unknown [Bacillus subtilis] >gi_2632358_emb_CAB11867 (Z99104) similar to hypothetical proteins [Bacillus subtilis]
Seq. No.	7541
Contig ID	9601_1.R1040
5'-most EST	epx701107762.h1
Seq. No.	7542
Contig ID	9603_1.R1040
5'-most EST	jC-gmle01810089e12d1
Seq. No.	7543
Contig ID	9606_1.R1040
5'-most EST	leu701152657.h1
Method	BLASTX
NCBI GI	g4455202
BLAST score	405
E value	2.0e-39
Match length	114
% identity	73
NCBI Description	(AL035440) putative APG protein [Arabidopsis thaliana]
Seq. No.	7544
Contig ID	9610_1.R1040
5'-most EST	rlr700901982.h1
Method	BLASTX
NCBI GI	g4559310
BLAST score	154
E value	1.0e-09
Match length	119
% identity	31
NCBI Description	(AF129131) putative Zic3 binding protein; CBP3 protein homolog [Xenopus laevis]
Seq. No.	7545
Contig ID	9626_1.R1040
5'-most EST	gsv701051404.h1
Method	BLASTX
NCBI GI	g2194122
BLAST score	221
E value	1.0e-17

09684016-101000

Match length 151
% identity 40
NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]

Seq. No. 7546
Contig ID 9626_2.R1040
5'-most EST LIB3051-020-Q1-E1-G3
Method BLASTX
NCBI GI g3123176
BLAST score 287
E value 4.0e-25
Match length 249
% identity 22
NCBI Description HYPOTHETICAL 43.1 KD TRP-ASP REPEATS CONTAINING PROTEIN K04G11.4 IN CHROMOSOME X >gi_3878300_emb_CAB01760_ (Z78544) predicted using Genefinder; Similarity to C.elegans Guanine nucleotide binding protein (WP:C14B1.4) [Caenorhabditis elegans]

Seq. No. 7547
Contig ID 9626_3.R1040
5'-most EST LIB3039-018-Q1-E1-E3
Method BLASTX
NCBI GI g3451472
BLAST score 155
E value 1.0e-09
Match length 112
% identity 9
NCBI Description (AL031349) transcription initiation factor TFIID subunit [Schizosaccharomyces pombe]

Seq. No. 7548
Contig ID 9626_6.R1040
5'-most EST jC-gmle01810035d06d1

Seq. No. 7549
Contig ID 9630_1.R1040
5'-most EST jC-gmf102220114c12a1
Method BLASTX
NCBI GI g3367537
BLAST score 372
E value 4.0e-35
Match length 137
% identity 54
NCBI Description (AC004392) Contains similarity to ANK repeat region of Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107 from Caenorhabditis elegans cosmid gb_U00049. This gene is continued from unannotated gene on BAC F19K23 gb_AC000375. [Arabid

Seq. No. 7550
Contig ID 9638_1.R1040
5'-most EST LIB3039-018-Q1-E1-D1

Seq. No. 7551
Contig ID 9644_1.R1040
5'-most EST jC-gmf102220053a07a1

Seq. No. 7552
 Contig ID 9646 1.R1040
 5'-most EST LIB3039-018-Q1-E1-C2
 Method BLASTX
 NCBI GI g3451067
 BLAST score 189
 E value 2.0e-14
 Match length 44
 % identity 84
 NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 7553
 Contig ID 9665 1.R1040
 5'-most EST LIB3039-017-Q1-E1-H4

Seq. No. 7554
 Contig ID 9666 1.R1040
 5'-most EST LIB3039-017-Q1-E1-H5

Seq. No. 7555
 Contig ID 9672 1.R1040
 5'-most EST LIB3039-018-Q1-E1-A12
 Method BLASTX
 NCBI GI g632220
 BLAST score 315
 E value 6.0e-29
 Match length 112
 % identity 61
 NCBI Description ribosomal protein L2 - evening primrose mitochondrion
 >gi_516394_emb_CAA56451_ (X80170) 70s mitochondrial
 ribosomal protein L2 [Oenothera berteriana]

Seq. No. 7556
 Contig ID 9673 1.R1040
 5'-most EST LIB3039-018-Q1-E1-A3
 Method BLASTX
 NCBI GI g2253579
 BLAST score 141
 E value 9.0e-09
 Match length 83
 % identity 45
 NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7557
 Contig ID 9676 1.R1040
 5'-most EST LIB3039-017-Q1-E1-E3
 Method BLASTX
 NCBI GI g109219
 BLAST score 272
 E value 1.0e-23
 Match length 230
 % identity 34
 NCBI Description dimethylaniline monooxygenase (N-oxide-forming) (EC
 1.14.13.8), hepatic 1 - rabbit

Seq. No. 7558

% identity	73
NCBI Description	(AC005169) unknown protein [Arabidopsis thaliana]
Seq. No.	7581
Contig ID	9784_1.R1040
5'-most EST	LIB3107-003-Q1-K1-B10
Seq. No.	7582
Contig ID	9785_1.R1040
5'-most EST	xpa700795562.h1
Seq. No.	7583
Contig ID	9788_1.R1040
5'-most EST	g5606786
Method	BLASTX
NCBI GI	g4539390
BLAST score	1815
E value	0.0e+00
Match length	380
% identity	88
NCBI Description	(AL035526) shaggy-like protein kinase etha (EC 2.7.1.-) [Arabidopsis thaliana]
Seq. No.	7584
Contig ID	9788_2.R1040
5'-most EST	jC-gmst02400055c01a1
Method	BLASTX
NCBI GI	g4056456
BLAST score	686
E value	3.0e-72
Match length	204
% identity	69
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]
Seq. No.	7585
Contig ID	9788_3.R1040
5'-most EST	crh700851255.h1
Method	BLASTX
NCBI GI	g4539390
BLAST score	626
E value	4.0e-65
Match length	135
% identity	87
NCBI Description	(AL035526) shaggy-like protein kinase etha (EC 2.7.1.-) [Arabidopsis thaliana]
Seq. No.	7586
Contig ID	9788_4.R1040
5'-most EST	LIB3049-020-Q1-E1-B6
Method	BLASTX
NCBI GI	g2182029
BLAST score	579
E value	1.0e-61
Match length	148

% identity 84
 NCBI Description (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]

Seq. No. 7587
 Contig ID 9788_5.R1040
 5'-most EST xpa700792520.h1
 Method BLASTX
 NCBI GI g2129738
 BLAST score 560
 E value 1.0e-57
 Match length 141
 % identity 74
 NCBI Description shaggy-like kinase dzeta - Arabidopsis thaliana
 >gi_1225913_emb_CAA64408_(X94938) shaggy-like kinase dzeta
 [Arabidopsis thaliana] >gi_1669653_emb_CAA70483_(Y09300)
 serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 7588
 Contig ID 9788_6.R1040
 5'-most EST uC-gmflminsoy079c09b1

Seq. No. 7589
 Contig ID 9788_9.R1040
 5'-most EST LIB3170-024-Q1-J1-A12

Seq. No. 7590
 Contig ID 9788_11.R1040
 5'-most EST LIB3049-002-Q1-E1-G7
 Method BLASTX
 NCBI GI g1532168
 BLAST score 194
 E value 7.0e-15
 Match length 66
 % identity 59
 NCBI Description (U63815) localized according to blastn similarity to EST
 sequences; therefore, the coding span corresponds only to
 an area of similarity since the initiation codon and stop
 codon could not be precisely determined [Arabidopsis
 thaliana]

Seq. No. 7591
 Contig ID 9788_12.R1040
 5'-most EST uC-gmflminsoy069b05b1
 Method BLASTX
 NCBI GI g4539390
 BLAST score 413
 E value 2.0e-52
 Match length 119
 % identity 81
 NCBI Description (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-)
 [Arabidopsis thaliana]

Seq. No. 7592
 Contig ID 9788_13.R1040
 5'-most EST LIB3049-020-Q1-E1-B4
 Method BLASTX
 NCBI GI g1877397

09684016-101000

NCBI GI g2854153
 BLAST score 296
 E value 1.0e-35
 Match length 166
 % identity 51
 NCBI Description (AF045640) No definition line found [Caenorhabditis elegans]

Seq. No. 7600
 Contig ID 9807_2.R1040
 5'-most EST LIB3093-039-Q1-K1-A3
 Method BLASTX
 NCBI GI g2854153
 BLAST score 149
 E value 2.0e-09
 Match length 55
 % identity 56
 NCBI Description (AF045640) No definition line found [Caenorhabditis elegans]

Seq. No. 7601
 Contig ID 9811_1.R1040
 5'-most EST leu701154049.h1

Seq. No. 7602
 Contig ID 9813_1.R1040
 5'-most EST LIB3039-015-Q1-E1-D8

Seq. No. 7603
 Contig ID 9815_1.R1040
 5'-most EST trc700562769.h1
 Method BLASTX
 NCBI GI g3063710
 BLAST score 188
 E value 2.0e-13
 Match length 116
 % identity 34
 NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 7604
 Contig ID 9815_4.R1040
 5'-most EST jC-gmro02910019e01a1

Seq. No. 7605
 Contig ID 9818_1.R1040
 5'-most EST LIB3039-015-Q1-E1-C7
 Method BLASTX
 NCBI GI g3892050
 BLAST score 550
 E value 1.0e-81
 Match length 281
 % identity 67
 NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7606
 Contig ID 9830_1.R1040
 5'-most EST LIB3039-015-Q1-E1-B10

Seq. No. 7607
 Contig ID 9830_2.R1040
 5'-most EST LIB3106-095-Q1-K1-D6

Seq. No. 7608
 Contig ID 9830_3.R1040
 5'-most EST uC-gmflminsoy017c12b1

Seq. No. 7609
 Contig ID 9841_1.R1040
 5'-most EST hrw701062003.h1

Seq. No. 7610
 Contig ID 9858_1.R1040
 5'-most EST xpa700795673.h1
 Method BLASTX
 NCBI GI g1532175
 BLAST score 408
 E value 1.0e-39
 Match length 104
 % identity 68
 NCBI Description (U63815) similar to protein disulfide isomerase
 [Arabidopsis thaliana]

Seq. No. 7611
 Contig ID 9859_1.R1040
 5'-most EST LIB3039-001-Q1-E1-H4
 Method BLASTX
 NCBI GI g3128177
 BLAST score 508
 E value 3.0e-51
 Match length 136
 % identity 74
 NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 7612
 Contig ID 9859_2.R1040
 5'-most EST pcp700991855.h1
 Method BLASTX
 NCBI GI g3128177
 BLAST score 294
 E value 1.0e-26
 Match length 79
 % identity 73
 NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 7613
 Contig ID 9862_1.R1040
 5'-most EST gsv701048517.h1
 Method BLASTX
 NCBI GI g3236245
 BLAST score 635
 E value 7.0e-72
 Match length 241
 % identity 63
 NCBI Description (AC004684) myb-related protein [Arabidopsis thaliana]

5'-most EST uC-gmflminsoy037b04b1
 Method BLASTX
 NCBI GI g3273562
 BLAST score 255
 E value 8.0e-22
 Match length 104
 % identity 45
 NCBI Description (AF036707) RAD6 [Candida albicans]

Seq. No. 7624
 Contig ID 9915_1.R1040
 5'-most EST LIB3039-013-Q1-E1-F6
 Method BLASTX
 NCBI GI g285741
 BLAST score 152
 E value 6.0e-10
 Match length 79
 % identity 39
 NCBI Description (D14550) EDGP precursor [Daucus carota]

Seq. No. 7625
 Contig ID 9927_1.R1040
 5'-most EST LIB3107-040-Q1-K1-C1
 Method BLASTX
 NCBI GI g3024629
 BLAST score 201
 E value 2.0e-15
 Match length 137
 % identity 33
 NCBI Description GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-GAMMA)
 >gi_423252_pir_S32369 gamma-SNAP protein - bovine
 >gi_298669_bbs_127528 gamma soluble NSF attachment protein,
 gamma SNAP=N-ethyl-maleimide-sensitive fusion protein
 attachment protein [cattle, brain, Peptide, 328 aa]
 >gi_445846_prf_1910317C NSF attachment protein
 (SNAP):ISOTYPE=gamma [Bos taurus]

Seq. No. 7626
 Contig ID 9930_1.R1040
 5'-most EST LIB3139-107-P1-N1-B3
 Method BLASTX
 NCBI GI g2494113
 BLAST score 1038
 E value 1.0e-113
 Match length 226
 % identity 83
 NCBI Description (AC002376) Strong similarity to Musa pectate lyase
 (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come
 from this gene. [Arabidopsis thaliana]

Seq. No. 7627
 Contig ID 9933_1.R1040
 5'-most EST LIB3052-012-Q1-N1-B3

Seq. No. 7628
 Contig ID 9938_1.R1040
 5'-most EST sat701015315.h1

Method	BLASTX
NCBI GI	g4538965
BLAST score	250
E value	2.0e-21
Match length	105
% identity	47
NCBI Description	(AL049488) hypothetical protein [Arabidopsis thaliana]
Seq. No.	7629
Contig ID	9942_1.R1040
5'-most EST	LIB3170-055-Q1-K1-G2
Method	BLASTX
NCBI GI	g2494162
BLAST score	776
E value	2.0e-82
Match length	335
% identity	49
NCBI Description	HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR >gi_3879803_emb_CAA87414_ (Z47356) similar to DNAJ [Caenorhabditis elegans]
Seq. No.	7630
Contig ID	9942_4.R1040
5'-most EST	uC-gmrominsoy128f10b1
Method	BLASTX
NCBI GI	g144832
BLAST score	152
E value	6.0e-10
Match length	41
% identity	63
NCBI Description	(M74569) dnaJ [Clostridium acetobutylicum]
Seq. No.	7631
Contig ID	9944_1.R1040
5'-most EST	LIB3039-013-Q1-E1-B3
Seq. No.	7632
Contig ID	9944_2.R1040
5'-most EST	uC-gmflminsoy056e05b1
Seq. No.	7633
Contig ID	9948_1.R1040
5'-most EST	uC-gmrominsoy271a10b1
Seq. No.	7634
Contig ID	9948_2.R1040
5'-most EST	LIB3109-014-Q1-K1-B8
Seq. No.	7635
Contig ID	9949_1.R1040
5'-most EST	jC-gmro02800041h12a1
Method	BLASTX
NCBI GI	g2760362
BLAST score	647
E value	1.0e-67
Match length	138
% identity	89

5'-most EST LIB3074-026-Q1-E1-C4
 Method BLASTX
 NCBI GI g4309884
 BLAST score 116
 E value 2.0e-09
 Match length 68
 % identity 53
 NCBI Description (AC006389) similar to Schizosaccharomyces pombe splicing factor; similar to PID:3395591 [Homo sapiens]

Seq. No. 7642
 Contig ID 9958_1.R1040
 5'-most EST seb700649775.h1
 Method BLASTN
 NCBI GI g410285
 BLAST score 367
 E value 0.0e+00
 Match length 804
 % identity 90
 NCBI Description Pisum sativum rho (ras-related) GTP-binding protein mRNA, complete cds

Seq. No. 7643
 Contig ID 9958_3.R1040
 5'-most EST jC-gmst02400031h06a1
 Method BLASTN
 NCBI GI g410285
 BLAST score 90
 E value 7.0e-43
 Match length 186
 % identity 87
 NCBI Description Pisum sativum rho (ras-related) GTP-binding protein mRNA, complete cds

Seq. No. 7644
 Contig ID 9958_7.R1040
 5'-most EST eep700869546.h1
 Method BLASTN
 NCBI GI g410285
 BLAST score 42
 E value 2.0e-14
 Match length 62
 % identity 92
 NCBI Description Pisum sativum rho (ras-related) GTP-binding protein mRNA, complete cds

Seq. No. 7645
 Contig ID 9966_1.R1040
 5'-most EST asn701141112.h1

Seq. No. 7646
 Contig ID 9966_2.R1040
 5'-most EST LIB3039-012-Q1-E1-G10

Seq. No. 7647
 Contig ID 9967_1.R1040
 5'-most EST LIB3039-012-Q1-E1-G12

Method BLASTX
 NCBI GI g1330343
 BLAST score 312
 E value 8.0e-29
 Match length 99
 % identity 60
 NCBI Description (U58755) C34D4.12 gene product [Caenorhabditis elegans]

Seq. No. 7648
 Contig ID 9979_1.R1040
 5'-most EST LIB3092-018-Q1-K1-D12
 Method BLASTX
 NCBI GI g3212852
 BLAST score 387
 E value 2.0e-46
 Match length 176
 % identity 53
 NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 7649
 Contig ID 9988_1.R1040
 5'-most EST LIB3139-088-P1-N1-A7
 Method BLASTX
 NCBI GI g4240116
 BLAST score 844
 E value 9.0e-91
 Match length 189
 % identity 80
 NCBI Description (AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800)
 NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No. 7650
 Contig ID 9988_2.R1040
 5'-most EST LIB3039-012-Q1-E1-C10
 Method BLASTX
 NCBI GI g4336205
 BLAST score 362
 E value 2.0e-34
 Match length 104
 % identity 64
 NCBI Description (AF077372) cytochrome b5 reductase [Zea mays]

Seq. No. 7651
 Contig ID 9989_2.R1040
 5'-most EST zsg701128847.h1
 Method BLASTX
 NCBI GI g3894191
 BLAST score 423
 E value 2.0e-41
 Match length 158
 % identity 54
 NCBI Description (AC005662) unknown protein [Arabidopsis thaliana]

Seq. No. 7652
 Contig ID 9999_1.R1040
 5'-most EST LIB3039-012-Q1-E1-D1

Method BLASTX
 NCBI GI g4006867
 BLAST score 741
 E value 3.0e-81
 Match length 197
 % identity 81
 NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 7653
 Contig ID 10010_1.R1040
 5'-most EST ncj700979503.h2
 Method BLASTX
 NCBI GI g3860319
 BLAST score 1682
 E value 0.0e+00
 Match length 442
 % identity 77
 NCBI Description (AJ012686) nucleolar protein [Cicer arietinum]

Seq. No. 7654
 Contig ID 10010_2.R1040
 5'-most EST LIB3049-026-Q1-E1-F6
 Method BLASTX
 NCBI GI g4160346
 BLAST score 337
 E value 2.0e-31
 Match length 142
 % identity 50
 NCBI Description (AL035216) nucleolar protein involved in pre-rRNA processing [Schizosaccharomyces pombe]

Seq. No. 7655
 Contig ID 10010_3.R1040
 5'-most EST LIB3139-026-P1-N1-C1
 Method BLASTN
 NCBI GI g3860318
 BLAST score 135
 E value 1.0e-69
 Match length 281
 % identity 89
 NCBI Description Cicer arietinum mRNA for nucleolar protein, partial

Seq. No. 7656
 Contig ID 10018_1.R1040
 5'-most EST trc700565153.h1
 Method BLASTX
 NCBI GI g2462822
 BLAST score 354
 E value 4.0e-33
 Match length 148
 % identity 53
 NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7657
 Contig ID 10027_1.R1040
 5'-most EST jsh701063965.h1

[illegible][illegible][illegible][illegible]

	0	1	2	3	4	5	6	7	8	9	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	[\] ^ _ ` { } ~ ? , . / : ; " ' & * + = % & # \$ % &																									
0	00	01	02	03	04	05	06	07	08	09	0A	0B	0C	0D	0E	0F	0G	0H	0I	0J	0K	0L	0M	0N	0O	0P	0Q	0R	0S	0T	0U	0V	0W	0X	0Y	0Z	0[0\	0]	0^	0_	0`	0{	0	0}	0~	0?	0,	0.	0/	0:	0;	0"	0'	0&	0*	0+	0=	0%	0&	0#	0\$	0%	0&
1	10	11	12	13	14	15	16	17	18	19	1A	1B	1C	1D	1E	1F	1G	1H	1I	1J	1K	1L	1M	1N	1O	1P	1Q	1R	1S	1T	1U	1V	1W	1X	1Y	1Z	1[1\	1]	1^	1_	1`	1{	1	1}	1~	1?	1,	1.	1/	1:	1;	1"	1'	1&	1*	1+	1=	1%	1&	1#	1\$	1%	1&
2	20	21	22	23	24	25	26	27	28	29	2A	2B	2C	2D	2E	2F	2G	2H	2I	2J	2K	2L	2M	2N	2O	2P	2Q	2R	2S	2T	2U	2V	2W	2X	2Y	2Z	2[2\	2]	2^	2_	2`	2{	2	2}	2~	2?	2,	2.	2/	2:	2;	2"	2'	2&	2*	2+	2=	2%	2&	2#	2\$	2%	2&
3	30	31	32	33	34	35	36	37	38	39	3A	3B	3C	3D	3E	3F	3G	3H	3I	3J	3K	3L	3M	3N	3O	3P	3Q	3R	3S	3T	3U	3V	3W	3X	3Y	3Z	3[3\	3]	3^	3_	3`	3{	3	3}	3~	3?	3,	3.	3/	3:	3;	3"	3'	3&	3*	3+	3=	3%	3&	3#	3\$	3%	3&
4	40	41	42	43	44	45	46	47	48	49	4A	4B	4C	4D	4E	4F	4G	4H	4I	4J	4K	4L	4M	4N	4O	4P	4Q	4R	4S	4T	4U	4V	4W	4X	4Y	4Z	4[4\	4]	4^	4_	4`	4{	4	4}	4~	4?	4,	4.	4/	4:	4;	4"	4'	4&	4*	4+	4=	4%	4&	4#	4\$	4%	4&
5	50	51	52	53	54	55	56	57	58	59	5A	5B	5C	5D	5E	5F	5G	5H	5I	5J	5K	5L	5M	5N	5O	5P	5Q	5R	5S	5T	5U	5V	5W	5X	5Y	5Z	5[5\	5]	5^	5_	5`	5{	5	5}	5~	5?	5,	5.	5/	5:	5;	5"	5'	5&	5*	5+	5=	5%	5&	5#	5\$	5%	5&
6	60	61	62	63	64	65	66	67	68	69	6A	6B	6C	6D	6E	6F	6G	6H	6I	6J	6K	6L	6M	6N	6O	6P	6Q	6R	6S	6T	6U	6V	6W	6X	6Y	6Z	6[6\	6]	6^	6_	6`	6{	6	6}	6~	6?	6,	6.	6/	6:	6;	6"	6'	6&	6*	6+	6=	6%	6&	6#	6\$	6%	6&
7	70	71	72	73	74	75	76	77	78	79	7A	7B	7C	7D	7E	7F	7G	7H	7I	7J	7K	7L	7M	7N	7O	7P	7Q	7R	7S	7T	7U	7V	7W	7X	7Y	7Z	7[7\	7]	7^	7_	7`	7{	7	7}	7~	7?	7,	7.	7/	7:	7;	7"	7'	7&	7*	7+	7=	7%	7&	7#	7\$	7%	7&
8	80	81	82	83	84	85	86	87	88	89	8A	8B	8C	8D	8E	8F	8G	8H	8I	8J	8K	8L	8M	8N	8O	8P	8Q	8R	8S	8T	8U	8V	8W	8X	8Y																													

[illegible][illegible]

09634016 17 10100

Seq. No.	7666
Contig ID	10068_4.R1040
5'-most EST	zhf700964470.h1
Method	BLASTX
NCBI GI	g3876716
BLAST score	206
E value	2.0e-16
Match length	66
% identity	48
NCBI Description	(Z46242) simila

```
Seq. No.          7668
Contig ID         10071_2.R1040
5'-most EST      leu701157872.h1
Method            BLASTN
NCBI GI           g532289
BLAST score       49
E value           2.0e-18
Match length      61
% identity        95
NCBI Description   Soybean mRNA for late nodulin, complete cds
```

```
Seq. No.          7670
Contig ID         10073_1.R1040
5'-most EST      LIB3039-011-Q1-E1-B2
Method           BLASTX
NCBI GI          g2262104
BLAST score      439
E value          1.0e-43
Match length     121
% identity       69
NCBI Description  (AC002343) unknown protein [Arabidopsis thaliana]
```

1408

0000016101000

5'-most EST LIB3039-011-Q1-E1-B5

Seq. No. 7672
 Contig ID 10078_1.R1040
 5'-most EST gsv701053747.h1
 Method BLASTX
 NCBI GI g3021409
 BLAST score 212
 E value 8.0e-17
 Match length 70
 % identity 57
 NCBI Description (Y12781) transducin (beta) like 1 protein [Homo sapiens]

Seq. No. 7673
 Contig ID 10098_1.R1040
 5'-most EST LIB3051-005-Q1-E1-C6
 Method BLASTX
 NCBI GI g3193298
 BLAST score 214
 E value 2.0e-35
 Match length 137
 % identity 55
 NCBI Description (AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No. 7674
 Contig ID 10098_2.R1040
 5'-most EST zhf700955551.h1

Seq. No. 7675
 Contig ID 10100_1.R1040
 5'-most EST LIB3039-010-Q1-E1-G5
 Method BLASTN
 NCBI GI g1732468
 BLAST score 64
 E value 2.0e-27
 Match length 136
 % identity 87
 NCBI Description Soybean mRNA for Mg chelatase subunit (46 kD), complete cds

Seq. No. 7676
 Contig ID 10105_1.R1040
 5'-most EST LIB3039-010-Q1-E1-E11
 Method BLASTX
 NCBI GI g3608154
 BLAST score 288
 E value 7.0e-26
 Match length 137
 % identity 43
 NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 7677
 Contig ID 10107_1.R1040
 5'-most EST LIB3053-002-Q1-B1-C4
 Method BLASTX
 NCBI GI g4539422
 BLAST score 1186
 E value 1.0e-130

Match length 80
 % identity 61
 NCBI Description (AL049171) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 7703
 Contig ID 10249_2.R1040
 5'-most EST uxk700672272.h1

Seq. No. 7704
 Contig ID 10250_1.R1040
 5'-most EST LIB3107-005-Q1-K1-F9
 Method BLASTX
 NCBI GI g3025188
 BLAST score 366
 E value 1.0e-34
 Match length 107
 % identity 61
 NCBI Description HYPOTHETICAL 11.9 KD PROTEIN SLR1846
 >gi_1652154_dbj_BAA17078_ (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 7705
 Contig ID 10261_1.R1040
 5'-most EST ncj700978977.h1
 Method BLASTX
 NCBI GI g1362615
 BLAST score 810
 E value 2.0e-86
 Match length 404
 % identity 44
 NCBI Description iswi protein - fruit fly (Drosophila melanogaster)
 >gi_439197 (L27127) ISWI protein [Drosophila melanogaster]

Seq. No. 7706
 Contig ID 10264_1.R1040
 5'-most EST LIB3039-008-Q1-E1-A10
 Method BLASTX
 NCBI GI g2760326
 BLAST score 145
 E value 3.0e-09
 Match length 88
 % identity 34
 NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No. 7707
 Contig ID 10269_1.R1040
 5'-most EST gsv701044623.h1
 Method BLASTX
 NCBI GI g2911799
 BLAST score 724
 E value 1.0e-76
 Match length 222
 % identity 61
 NCBI Description (AF008184) 4-coumarate:CoA ligase 1 [Populus balsamifera subsp. trichocarpa X Populus deltoides]

0000707 9048550

Contig ID 10410_2.R1040
5'-most EST LIB3039-005-Q1-E1-D11
Method BLASTX
NCBI GI g3121825
BLAST score 619
E value 2.0e-64
Match length 182
% identity 70
NCBI Description 2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No. 7739
Contig ID 10418_1.R1040
5'-most EST LIB3039-005-Q1-E1-B10
Method BLASTN
NCBI GI g1495767
BLAST score 238
E value 1.0e-131
Match length 611
% identity 84
NCBI Description P.sativum mRNA for 110 kD chloroplast inner envelope protein IEP110

Seq. No. 7740
Contig ID 10425_1.R1040
5'-most EST leu701157388.h1
Method BLASTX
NCBI GI g2897942
BLAST score 317
E value 7.0e-29
Match length 165
% identity 42
NCBI Description (AF003938) thioredoxin-like protein [Homo sapiens]
>gi_2961254 (AF051896) thioredoxin homolog [Homo sapiens]
>gi_2970689 (AF052659) thioredoxin-related protein [Homo sapiens]

Seq. No. 7741
Contig ID 10428_1.R1040
5'-most EST LIB3049-026-Q1-E1-G3
Method BLASTX
NCBI GI g4538959
BLAST score 460
E value 7.0e-46
Match length 105
% identity 80
NCBI Description (AL049488) putative protein [Arabidopsis thaliana]

Seq. No. 7742
Contig ID 10430_1.R1040
5'-most EST LIB3039-004-Q1-E1-H1

Seq. No. 7743
Contig ID 10432_1.R1040
5'-most EST rlr700902245.h1
Method BLASTX

NCBI GI	g2618688
BLAST score	681
E value	1.0e-71
Match length	157
% identity	82
NCBI Description	(AC002510) putative esterase D [Arabidopsis thaliana]
Seq. No.	7744
Contig ID	10435_1.R1040
5'-most EST	LIB3051-116-Q1-K1-A2
Seq. No.	7745
Contig ID	10439_1.R1040
5'-most EST	leu701144983.h1
Method	BLASTX
NCBI GI	g4191782
BLAST score	2171
E value	0.0e+00
Match length	503
% identity	82
NCBI Description	(AC005917) WD-40 repeat protein [Arabidopsis thaliana]
Seq. No.	7746
Contig ID	10449_1.R1040
5'-most EST	LIB3039-004-Q1-E1-D9
Method	BLASTX
NCBI GI	g4263517
BLAST score	199
E value	2.0e-31
Match length	112
% identity	64
NCBI Description	(AC004044) similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana]
Seq. No.	7747
Contig ID	10453_1.R1040
5'-most EST	LIB3040-043-Q1-E1-H7
Method	BLASTX
NCBI GI	g4406774
BLAST score	920
E value	2.0e-99
Match length	264
% identity	64
NCBI Description	(AC006836) putative nonsense-mediated mRNA decay protein, 5' partial [Arabidopsis thaliana]
Seq. No.	7748
Contig ID	10458_1.R1040
5'-most EST	seb700652912.h1
Method	BLASTX
NCBI GI	g3138972
BLAST score	258
E value	3.0e-22
Match length	67
% identity	73

NCBI GI	g1184122
BLAST score	346
E value	0.0e+00
Match length	650
% identity	88
NCBI Description	Vigna radiata clone MII-4 auxin-induced protein mRNA, partial cds
Seq. No.	7798
Contig ID	10646_3.R1040
5'-most EST	LIB3039-001-Q1-E1-E9
Method	BLASTN
NCBI GI	g169980
BLAST score	431
E value	0.0e+00
Match length	1070
% identity	93
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.	7799
Contig ID	10646_4.R1040
5'-most EST	zsg701126407.hl
Method	BLASTN
NCBI GI	g169980
BLAST score	225
E value	1.0e-123
Match length	369
% identity	92
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.	7800
Contig ID	10646_5.R1040
5'-most EST	rlr700900057.hl
Method	BLASTN
NCBI GI	g169980
BLAST score	188
E value	1.0e-101
Match length	509
% identity	88
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.	7801
Contig ID	10646_6.R1040
5'-most EST	LIB3094-051-Q1-K1-A4
Method	BLASTN
NCBI GI	g169980
BLAST score	217
E value	1.0e-118
Match length	347
% identity	94
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.	7802
Contig ID	10648_1.R1040
5'-most EST	LIB3039-001-Q1-E1-C4
Method	BLASTN
NCBI GI	q1518539

09684015.101000

Method BLASTN
NCBI GI g456713
BLAST score 608
E value 0.0e+00
Match length 739
% identity 69
NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No. 7818
Contig ID 10699_2.R1040
5'-most EST LIB3040-024-Q1-E1-H12
Method BLASTN
NCBI GI g303900
BLAST score 369
E value 0.0e+00
Match length 586
% identity 61
NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No. 7819
Contig ID 10701_1.R1040
5'-most EST LIB3039-009-Q1-E1-G5
Method BLASTX
NCBI GI g2129630
BLAST score 246
E value 6.0e-21
Match length 91
% identity 44
NCBI Description lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750
(X97023) lamin [Arabidopsis thaliana] >gi_3395760 (U77721)
unknown [Arabidopsis thaliana]

Seq. No. 7820
Contig ID 10701_2.R1040
5'-most EST LIB3109-001-Q1-K1-H8
Method BLASTX
NCBI GI g2129630
BLAST score 150
E value 1.0e-09
Match length 51
% identity 49
NCBI Description lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750
(X97023) lamin [Arabidopsis thaliana] >gi_3395760 (U77721)
unknown [Arabidopsis thaliana]

Seq. No. 7821
Contig ID 10703_1.R1040
5'-most EST leu701146671.h1
Method BLASTX
NCBI GI g2760334
BLAST score 392
E value 1.0e-37
Match length 90
% identity 76
NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana]

Seq. No. 7822

Contig ID 10710_1.R1040
5'-most EST LIB3039-014-Q1-E1-C6

Seq. No. 7823
Contig ID 10718_1.R1040
5'-most EST LIB3065-024-Q1-N1-B1
Method BLASTX
NCBI GI g3372233
BLAST score 827
E value 1.0e-88
Match length 205
% identity 77
NCBI Description (AF019248) RNA polymerase I, II and III 24.3 kDa subunit
[Arabidopsis thaliana]

Seq. No. 7824
Contig ID 10718_3.R1040
5'-most EST jsh701068423.h1
Method BLASTX
NCBI GI g3372233
BLAST score 147
E value 2.0e-09
Match length 30
% identity 93
NCBI Description (AF019248) RNA polymerase I, II and III 24.3 kDa subunit
[Arabidopsis thaliana]

Seq. No. 7825
Contig ID 10733_2.R1040
5'-most EST LIB3139-057-P1-N1-B12

Seq. No. 7826
Contig ID 10743_1.R1040
5'-most EST LIB3087-002-Q1-K1-G10
Method BLASTX
NCBI GI g4406807
BLAST score 691
E value 1.0e-72
Match length 212
% identity 66
NCBI Description (AC006201) putative elongation factor beta-1 [Arabidopsis
thaliana]

Seq. No. 7827
Contig ID 10746_1.R1040
5'-most EST LIB3039-030-Q1-E1-H10
Method BLASTX
NCBI GI g4314355
BLAST score 685
E value 5.0e-72
Match length 207
% identity 58
NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]

Seq. No. 7828
Contig ID 10754_1.R1040
5'-most EST LIB3039-036-Q1-E1-A1

09684016-101000

Method	BLASTX
NCBI GI	g2586123
BLAST score	787
E value	6.0e-84
Match length	192
% identity	75
NCBI Description	(U89511) b-keto acyl reductase [Allium porrum]
Seq. No.	7829
Contig ID	10762_1.R1040
5'-most EST	LIB3039-038-Q1-E1-E5
Method	BLASTX
NCBI GI	g1408294
BLAST score	306
E value	2.0e-27
Match length	218
% identity	36
NCBI Description	(U61983) benzyl alcohol dehydrogenase [Acinetobacter calcoaceticus]
Seq. No.	7830
Contig ID	10767_1.R1040
5'-most EST	LIB3040-052-Q1-E1-D3
Method	BLASTX
NCBI GI	g4335763
BLAST score	424
E value	3.0e-41
Match length	161
% identity	50
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.	7831
Contig ID	10767_2.R1040
5'-most EST	fua701040645.h1
Seq. No.	7832
Contig ID	10768_1.R1040
5'-most EST	epx701106195.h1
Method	BLASTX
NCBI GI	g4098517
BLAST score	684
E value	6.0e-72
Match length	180
% identity	72
NCBI Description	(U79114) auxin-binding protein ABP19 [Prunus persica]
Seq. No.	7833
Contig ID	10771_1.R1040
5'-most EST	kl1701211959.h1
Seq. No.	7834
Contig ID	10771_2.R1040
5'-most EST	vzy700754421.h1
Seq. No.	7835
Contig ID	10779_1.R1040
5'-most EST	epx701105157.h1

Method BLASTX
 NCBI GI g119931
 BLAST score 443
 E value 1.0e-43
 Match length 146
 % identity 64
 NCBI Description FERREDOXIN I PRECURSOR >gi_65740_pir_FEPM1 ferredoxin
 [2Fe-2S] I precursor - garden pea >gi_169087 (M31713)
 ferredoxin I precursor [Pisum sativum]

Seq. No. 7836
 Contig ID 10783_1.R1040
 5'-most EST LIB3049-041-Q1-E1-A4
 Method BLASTX
 NCBI GI g3861188
 BLAST score 267
 E value 6.0e-23
 Match length 103
 % identity 54
 NCBI Description (AJ235272) 50S RIBOSOMAL PROTEIN L24 (rplX) [Rickettsia
 prowazekii]

Seq. No. 7837
 Contig ID 10783_2.R1040
 5'-most EST LIB3049-041-Q1-E1-G6
 Method BLASTX
 NCBI GI g3861188
 BLAST score 245
 E value 1.0e-20
 Match length 89
 % identity 53
 NCBI Description (AJ235272) 50S RIBOSOMAL PROTEIN L24 (rplX) [Rickettsia
 prowazekii]

Seq. No. 7838
 Contig ID 10783_3.R1040
 5'-most EST LIB3049-039-Q1-E1-A9
 Method BLASTX
 NCBI GI g143448
 BLAST score 181
 E value 2.0e-13
 Match length 75
 % identity 51
 NCBI Description (M81749) ribosomal protein L24 [Bacillus subtilis]

Seq. No. 7839
 Contig ID 10792_1.R1040
 5'-most EST jex700909892.h1
 Method BLASTX
 NCBI GI g2623298
 BLAST score 565
 E value 3.0e-58
 Match length 158
 % identity 70
 NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis
 thaliana]

[illegible]

100-46879-10

100-46879-10

100-46879-10

100-46879-10

100-46879-10

100-46879-10

E value 8.0e-27
 Match length 75
 % identity 75
 NCBI Description (AC004561) unknown protein [Arabidopsis thaliana]

Seq. No. 7853
 Contig ID 10830_1.R1040
 5'-most EST LIB3094-017-Q1-K1-A5
 Method BLASTN
 NCBI GI g3694834
 BLAST score 436
 E value 0.0e+00
 Match length 499
 % identity 98
 NCBI Description Glycine max alcohol dehydrogenase Adh-1 gene, partial cds

Seq. No. 7854
 Contig ID 10830_2.R1040
 5'-most EST uC-gmropic091g04b1
 Method BLASTN
 NCBI GI g452768
 BLAST score 319
 E value 1.0e-179
 Match length 451
 % identity 93
 NCBI Description P.acutifolius alcohol dehydrogenase-1F mRNA, complete CDS

Seq. No. 7855
 Contig ID 10830_3.R1040
 5'-most EST LIB3094-022-Q1-K1-C9
 Method BLASTN
 NCBI GI g3694834
 BLAST score 209
 E value 1.0e-114
 Match length 423
 % identity 97
 NCBI Description Glycine max alcohol dehydrogenase Adh-1 gene, partial cds

Seq. No. 7856
 Contig ID 10830_6.R1040
 5'-most EST uC-gmrominsoy039g09b1
 Method BLASTN
 NCBI GI g4039114
 BLAST score 435
 E value 0.0e+00
 Match length 493
 % identity 96
 NCBI Description Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds

Seq. No. 7857
 Contig ID 10838_1.R1040
 5'-most EST LIB3040-061-Q1-E11-A6

Seq. No. 7858
 Contig ID 10838_2.R1040
 5'-most EST jC-gmst02400027d03d1

% identity 50
NCBI Description hypothetical protein 1244 - common tobacco chloroplast

Seq. No. 7868
Contig ID 10864_1.R1040
5'-most EST LIB3167-023-P4-K4-G3
Method BLASTX
NCBI GI g3600061
BLAST score 262
E value 3.0e-22
Match length 172
% identity 40

NCBI Description (AF080120) contains similarity to DNA binding proteins [Arabidopsis thaliana]

Seq. No. 7869
Contig ID 10867_1.R1040
5'-most EST LIB3107-035-Q1-K1-G5
Method BLASTX
NCBI GI g3915961
BLAST score 1582
E value 0.0e+00
Match length 559
% identity 88

NCBI Description HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
>gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical protein [Nicotiana tabacum]

Seq. No. 7870
Contig ID 10867_2.R1040
5'-most EST LIB3170-005-Q1-K1-E11
Method BLASTN
NCBI GI g2924257
BLAST score 126
E value 3.0e-64
Match length 230
% identity 46

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 7871
Contig ID 10868_1.R1040
5'-most EST uC-gmflminsoy080h03b1

Seq. No. 7872
Contig ID 10873_1.R1040
5'-most EST LIB3040-018-Q1-E1-A11
Method BLASTX
NCBI GI g3582335
BLAST score 844
E value 1.0e-120
Match length 297
% identity 74

NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 7873
Contig ID 10873_2.R1040

Seq. No. 7886
Contig ID 10907_1.R1040
5'-most EST LIB3170-019-Q1-J1-D3

Seq. No. 7887
Contig ID 10912_1.R1040
5'-most EST LIB3170-011-Q1-K1-E9

Seq. No. 7888
Contig ID 10915_1.R1040
5'-most EST zhf700964946.h1
Method BLASTX
NCBI GI g2961378
BLAST score 1482
E value 1.0e-165
Match length 473
% identity 37
NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 7889
Contig ID 10915_2.R1040
5'-most EST uaw700664257.h1
Method BLASTX
NCBI GI g2961378
BLAST score 271
E value 9.0e-24
Match length 69
% identity 35
NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 7890
Contig ID 10917_1.R1040
5'-most EST uC-gmropic040d12b1
Method BLASTX
NCBI GI g1397319
BLAST score 209
E value 3.0e-16
Match length 118
% identity 38
NCBI Description (U61953) No definition line found [Caenorhabditis elegans]

Seq. No. 7891
Contig ID 10917_2.R1040
5'-most EST LIB3040-060-Q1-E1-C8

Seq. No. 7892
Contig ID 10920_1.R1040
5'-most EST LIB3040-060-Q1-E1-D2
Method BLASTX
NCBI GI g3193303
BLAST score 234
E value 2.0e-19
Match length 90
% identity 47
NCBI Description (AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis

thaliana]

Seq. No. 7893
 Contig ID 10923_1.R1040
 5'-most EST LIB3051-085-Q1-K1-G4
 Method BLASTX
 NCBI GI g2347194
 BLAST score 210
 E value 4.0e-18
 Match length 182
 % identity 36
 NCBI Description (AC002338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7894
 Contig ID 10929_1.R1040
 5'-most EST LIB3040-052-Q1-E1-H11
 Method BLASTX
 NCBI GI g3810855
 BLAST score 216
 E value 5.0e-17
 Match length 142
 % identity 39
 NCBI Description (AL032684) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 7895
 Contig ID 10931_1.R1040
 5'-most EST LIB3170-019-Q1-J1-C10

Seq. No. 7896
 Contig ID 10935_1.R1040
 5'-most EST zpv700762884.h1
 Method BLASTX
 NCBI GI g1076316
 BLAST score 296
 E value 1.0e-26
 Match length 121
 % identity 45
 NCBI Description drought-induced protein Di19 - Arabidopsis thaliana
 >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No. 7897
 Contig ID 10936_1.R1040
 5'-most EST LIB3092-056-Q1-K1-G4
 Method BLASTX
 NCBI GI g3582335
 BLAST score 1852
 E value 0.0e+00
 Match length 375
 % identity 91
 NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 7898
 Contig ID 10936_3.R1040
 5'-most EST LIB3170-002-Q1-J1-H4
 Method BLASTX
 NCBI GI g3582335

Seq. No. 7908
 Contig ID 10954_1.R1040
 5'-most EST LIB3051-044-Q1-K1-B3
 Method BLASTX
 NCBI GI g2583133
 BLAST score 247
 E value 1.0e-20
 Match length 179
 % identity 36
 NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]

Seq. No. 7909
 Contig ID 10954_2.R1040
 5'-most EST LIB3109-028-Q1-K1-D4

Seq. No. 7910
 Contig ID 10954_3.R1040
 5'-most EST leu701148605.h1

Seq. No. 7911
 Contig ID 10957_1.R1040
 5'-most EST leu701146515.h1
 Method BLASTX
 NCBI GI g2191136
 BLAST score 173
 E value 2.0e-16
 Match length 176
 % identity 34
 NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No. 7912
 Contig ID 10957_2.R1040
 5'-most EST LIB3040-045-Q1-E1-F2
 Method BLASTX
 NCBI GI g2191136
 BLAST score 177
 E value 7.0e-13
 Match length 100
 % identity 37
 NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No. 7913
 Contig ID 10962_1.R1040
 5'-most EST LIB3040-053-Q1-E1-A11
 Method BLASTN
 NCBI GI g313026
 BLAST score 67
 E value 4.0e-29
 Match length 195
 % identity 84

NCBI GI g4263713
 BLAST score 593
 E value 5.0e-61
 Match length 200
 % identity 58
 NCBI Description (AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7922
 Contig ID 10994_3.R1040
 5'-most EST jex700903123.h1
 Method BLASTX
 NCBI GI g4263713
 BLAST score 289
 E value 4.0e-26
 Match length 70
 % identity 71
 NCBI Description (AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7923
 Contig ID 10996_1.R1040
 5'-most EST LIB3040-046-Q1-E1-D5
 Method BLASTX
 NCBI GI g2583135
 BLAST score 578
 E value 2.0e-59
 Match length 159
 % identity 71
 NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]
 >gi_3822216 (AF074948) FIL [Arabidopsis thaliana]
 >gi_4322477_gb_AAD16053_ (AF087015) abnormal floral organs
 protein [Arabidopsis thaliana]

Seq. No. 7924
 Contig ID 10996_2.R1040
 5'-most EST LIB3170-001-Q1-K1-B1
 Method BLASTX
 NCBI GI g2583135
 BLAST score 348
 E value 7.0e-33
 Match length 115
 % identity 65
 NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]
 >gi_3822216 (AF074948) FIL [Arabidopsis thaliana]
 >gi_4322477_gb_AAD16053_ (AF087015) abnormal floral organs
 protein [Arabidopsis thaliana]

Seq. No. 7925
 Contig ID 11001_1.R1040
 5'-most EST uC-gmropic062a09b1

Seq. No. 7926
 Contig ID 11002_1.R1040
 5'-most EST uC-gmflminsoy046e01b1
 Method BLASTX
 NCBI GI g2464880
 BLAST score 372
 E value 2.0e-35

% identity	75
NCBI Description	(AC004138) putative expansin [Arabidopsis thaliana]
Seq. No.	7934
Contig ID	11017_2.R1040
5'-most EST	fC-gmse700658228z1
Method	BLASTX
NCBI GI	g4027897
BLAST score	268
E value	4.0e-23
Match length	55
% identity	84
NCBI Description	(AF049353) alpha-expansin precursor [Nicotiana tabacum]
Seq. No.	7935
Contig ID	11017_3.R1040
5'-most EST	LIB3040-058-Q1-E1-F4
Method	BLASTX
NCBI GI	g4027897
BLAST score	706
E value	1.0e-74
Match length	162
% identity	79
NCBI Description	(AF049353) alpha-expansin precursor [Nicotiana tabacum]
Seq. No.	7936
Contig ID	11018_1.R1040
5'-most EST	LIB3040-060-Q1-E1-A3
Method	BLASTX
NCBI GI	g2253442
BLAST score	260
E value	3.0e-22
Match length	62
% identity	66
NCBI Description	(AF007784) LTCOR11 [Lavatera thuringiaca]
Seq. No.	7937
Contig ID	11019_1.R1040
5'-most EST	uC-gmrominsoy277b05b1
Method	BLASTX
NCBI GI	g4158232
BLAST score	1716
E value	0.0e+00
Match length	332
% identity	92
NCBI Description	(Y18626) reversibly glycosylated polypeptide [Triticum aestivum]
Seq. No.	7938
Contig ID	11019_2.R1040
5'-most EST	kl1701204287.h2
Method	BLASTN
NCBI GI	g2218151
BLAST score	228
E value	1.0e-125
Match length	404
% identity	89

Seq. No. 7951
 Contig ID 11053_1.R1040
 5'-most EST g5753161

Seq. No. 7952
 Contig ID 11060_1.R1040
 5'-most EST LIB3072-053-Q1-E1-G11
 Method BLASTX
 NCBI GI g126078
 BLAST score 277
 E value 2.0e-24
 Match length 117
 % identity 30

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)
 >gi_81554_pir_S04046 embryonic abundant protein gD-34 -
 upland cotton >gi_18501_emb_CAA31594_ (X13206) D-34 Lea
 protein [Gossypium hirsutum] >gi_167385 (M19389) storage
 protein [Gossypium hirsutum] >gi_226556_prf_1601521F Lea
 D-34 gene [Saguinus oedipus]

Seq. No. 7953
 Contig ID 11061_1.R1040
 5'-most EST LIB3040-044-Q1-E1-A3
 Method BLASTX
 NCBI GI g2244822
 BLAST score 328
 E value 1.0e-30
 Match length 85
 % identity 72

NCBI Description (Z97336) RNA polymerase II fifth largest subunit homolog
 [Arabidopsis thaliana]

Seq. No. 7954
 Contig ID 11063_1.R1040
 5'-most EST LIB3092-008-Q1-K1-D1
 Method BLASTN
 NCBI GI g4104973
 BLAST score 491
 E value 0.0e+00
 Match length 895
 % identity 89

NCBI Description Pisum sativum spermidine synthase 2 (SPDSYN2) mRNA,
 complete cds

Seq. No. 7955
 Contig ID 11063_2.R1040
 5'-most EST LIB3052-014-Q1-N1-H2
 Method BLASTN
 NCBI GI g4104971
 BLAST score 205
 E value 1.0e-111
 Match length 347
 % identity 90

NCBI Description Pisum sativum spermidine synthase 1 (SPDSYN1) mRNA,
 complete cds

Seq. No. 7966
 Contig ID 11077_1.R1040
 5'-most EST LIB3170-017-Q1-J1-A12

Seq. No. 7967
 Contig ID 11082_1.R1040
 5'-most EST LIB3040-057-Q1-E1-E9

Seq. No. 7968
 Contig ID 11083_1.R1040
 5'-most EST LIB3040-031-Q1-E2-C12
 Method BLASTX
 NCBI GI g3283409
 BLAST score 165
 E value 4.0e-11
 Match length 58
 % identity 59
 NCBI Description (AF068754) heat shock factor binding protein 1 HSBP1 [Homo sapiens] >gi_4557647_ref_NP_001528.1_pHSBP1_heat shock factor binding protein

Seq. No. 7969
 Contig ID 11085_1.R1040
 5'-most EST LIB3074-036-Q1-K1-E2
 Method BLASTX
 NCBI GI g2739375
 BLAST score 268
 E value 2.0e-23
 Match length 107
 % identity 55
 NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 7970
 Contig ID 11085_3.R1040
 5'-most EST LIB3106-094-Q1-K1-F3
 Method BLASTX
 NCBI GI g2739375
 BLAST score 152
 E value 4.0e-10
 Match length 46
 % identity 67
 NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 7971
 Contig ID 11093_1.R1040
 5'-most EST LIB3106-057-Q1-K1-G9
 Method BLASTN
 NCBI GI g3603400
 BLAST score 455
 E value 0.0e+00
 Match length 1073
 % identity 86
 NCBI Description Medicago sativa cinnamyl-alcohol dehydrogenase (MsaCad1) mRNA, complete cds

Seq. No. 7972

Contig ID 11093_3.R1040
 5'-most EST zhf700954121.h1
 Method BLASTN
 NCBI GI g556421
 BLAST score 114
 E value 3.0e-57
 Match length 274
 % identity 85
 NCBI Description Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1) mRNA, complete cds

Seq. No. 7973
 Contig ID 11095_1.R1040
 5'-most EST LIB3040-057-Q1-E1-G2

Seq. No. 7974
 Contig ID 11100_1.R1040
 5'-most EST LIB3170-018-Q1-J1-A3

Seq. No. 7975
 Contig ID 11102_1.R1040
 5'-most EST LIB3107-042-Q1-K1-C6
 Method BLASTX
 NCBI GI g3738328
 BLAST score 315
 E value 5.0e-29
 Match length 79
 % identity 72
 NCBI Description (AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 7976
 Contig ID 11102_2.R1040
 5'-most EST LIB3040-057-Q1-E1-D3
 Method BLASTX
 NCBI GI g4263777
 BLAST score 234
 E value 1.0e-19
 Match length 84
 % identity 55
 NCBI Description (AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No. 7977
 Contig ID 11103_1.R1040
 5'-most EST LIB3040-057-Q1-E1-D5
 Method BLASTX
 NCBI GI g3004550
 BLAST score 176
 E value 2.0e-12
 Match length 64
 % identity 50
 NCBI Description (AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No. 7978
 Contig ID 11109_1.R1040

5'-most EST LIB3040-057-Q1-E1-E11
 Method BLASTX
 NCBI GI g586079
 BLAST score 1015
 E value 1.0e-111
 Match length 196
 % identity 97
 NCBI Description TUBULIN GAMMA-1 CHAIN >gi_460089 (U02069) g1-tubulin
 [Arabidopsis thaliana]

Seq. No. 7979
 Contig ID 11114_1.R1040
 5'-most EST LIB3040-057-Q1-E1-B1

Seq. No. 7980
 Contig ID 11120_1.R1040
 5'-most EST LIB3107-059-Q1-K1-D10
 Method BLASTX
 NCBI GI g266410
 BLAST score 378
 E value 4.0e-36
 Match length 144
 % identity 62
 NCBI Description CDC2+/CDC28-RELATED PROTEIN KINASE R2 >gi_82507_pir_S13934
 protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog -
 rice >gi_20194_emb_CAA41172_ (X58194) cdc2+/CDC28-related
 protein kinase [Oryza sativa]

Seq. No. 7981
 Contig ID 11122_1.R1040
 5'-most EST LIB3170-017-Q1-J1-A1

Seq. No. 7982
 Contig ID 11126_1.R1040
 5'-most EST LIB3170-020-Q1-K1-A12

Seq. No. 7983
 Contig ID 11127_1.R1040
 5'-most EST LIB3040-057-Q1-E1-C4
 Method BLASTX
 NCBI GI g4508075
 BLAST score 639
 E value 2.0e-66
 Match length 339
 % identity 44
 NCBI Description (AC005882) 50259 [Arabidopsis thaliana]

Seq. No. 7984
 Contig ID 11128_1.R1040
 5'-most EST LIB3139-062-P1-N1-H1
 Method BLASTX
 NCBI GI g2388956
 BLAST score 629
 E value 2.0e-65
 Match length 223
 % identity 58
 NCBI Description (Z98979) ribulose-phosphate 3-epimerase

[illegible]

Seq. No.	7994
Contig ID	11172_1.R1040
5'-most EST	LIB3049-008-Q1-E1-A6

00664016-101000

Match length 50
% identity 80
NCBI Description (AC006593) unknown protein [Arabidopsis thaliana]

Seq. No. 8008
Contig ID 11217_1.R1040
5'-most EST sat701010626.h1
Method BLASTX
NCBI GI g3786001
BLAST score 478
E value 2.0e-85
Match length 200
% identity 78
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 8009
Contig ID 11218_1.R1040
5'-most EST LIB3040-055-Q1-E1-F10
Method BLASTX
NCBI GI g2335098
BLAST score 1103
E value 1.0e-121
Match length 331
% identity 63
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 8010
Contig ID 11223_1.R1040
5'-most EST LIB3040-055-Q1-E1-F7
Method BLASTX
NCBI GI g4165861
BLAST score 187
E value 6.0e-14
Match length 83
% identity 46
NCBI Description (AF006603) histone deacetylase mHDA2 [Mus musculus]

Seq. No. 8011
Contig ID 11231_1.R1040
5'-most EST LIB3040-055-Q1-E1-C3

Seq. No. 8012
Contig ID 11233_1.R1040
5'-most EST jC-gmro02910068a07a1
Method BLASTX
NCBI GI g4049341
BLAST score 204
E value 9.0e-16
Match length 71
% identity 54
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 8013
Contig ID 11235_1.R1040
5'-most EST LIB3040-055-Q1-E1-D1

Seq. No. 8014

Seq. No.	8039
Contig ID	11336_1.R1040
5'-most EST	LIB3051-047-O1-K1-D3

Seq. No.	8040
Contig ID	11336_2.R1040
5'-most EST	uC-gmflminsoy008d12b1

Seq. No.	8041
Contig ID	11336_3.R1040
5'-most EST	LIB3040-045-Q1-E1-C3

Seq. No.	8042
Contig ID	11341_1.R1040
5'-most EST	LIB3040-053-O1-E1-B7

Seq. No.	8043
Contig ID	11343_1.R1040
5'-most EST	kl1701206623.h1

Seq. No.	8044
Contig ID	11343_2.R1040
5'-most EST	ncj700983657.h1

Seq. No.	8045
Contig ID	11344_1.R1040
5'-most EST	jC-gmf102220100e03a1

Seq. No.	8046
Contig ID	11348_1.R1040
5'-most EST	LIB3040-053-Q1-E1-D11

```
Seq. No.          8047
Contig ID         11356_1.R1040
5'-most EST      LIB3040-052-Q1-E1-H6
Method            BLASTN
NCBI GI           g2244991
BLAST score       44
E value           1.0e-15
Match length      112
% identity        85
NCBI Description  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
```

```
Seq. No.      8048
Contig ID     11363_1.R1040
5'-most EST   LIB3139-050-P1-N1-F10
Method        BLASTX
NCBI GI       g4220477
BLAST score    383
E value        6.0e-37
Match length   154
% identity     58
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
```

Seq. No.	8049
Contig ID	11365 1.R1040

[illegible]

```
Seq. No.          8085
Contig ID         11497_2.R1040
5'-most EST      LIB3170-054-Q1-K1-G12
Method            BLASTX
NCBI GI           g2275216
BLAST score       231
E value           3.0e-19
Match length      64
% identity        67
NCBI Description  (AC002337) cytochrome c oxidase Vc subunit isolog
                  [Arabidopsis thaliana]
```

Seq. No.	8087
Contig ID	11505_1.R1040
5'-most EST	LIB3170-015-Q1-K1-E7

```
Seq. No.      8088
Contig ID     11513_1.R1040
5'-most EST   LIB3040-061-Q1-E11-G7
Method        BLASTX
NCBI GI       g3282674
BLAST score    414
E value       2.0e-40
Match length   99
% identity     77
NCBI Description (AF036684) CCAAT-box binding factor HAP3 homolog
                [Arabidopsis thaliana]
```

```
Seq. No.      8089
Contig ID     11513_2.R1040
5'-most EST   LIB3040-026-Q1-E1-C6
Method        BLASTX
NCBI GI       g3282674
BLAST score    322
E value       1.0e-29
Match length   72
% identity     85
NCBI Description (AF036684) CCAAT-box binding factor HAP3 homolog
                [Arabidopsis thaliana]
```


Seq. No.	8101
Contig ID	11561_1.R1040
5'-most EST	vzy700755696.hl
Method	BLASTX
NCBI GI	g2244939
BLAST score	203
E value	1.0e-24
Match length	181
% identity	44
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]
Seq. No.	8102
Contig ID	11562_1.R1040
5'-most EST	uaw700662405.hl
Seq. No.	8103
Contig ID	11562_3.R1040
5'-most EST	zpv700759748.hl
Seq. No.	8104
Contig ID	11569_1.R1040
5'-most EST	LIB3074-039-Q1-K1-F6
Method	BLASTX
NCBI GI	g4467116
BLAST score	312
E value	3.0e-28
Match length	134
% identity	46
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]
Seq. No.	8105
Contig ID	11570_1.R1040
5'-most EST	LIB3040-049-Q1-E1-E2
Seq. No.	8106
Contig ID	11571_1.R1040
5'-most EST	uC-gmrominsoy063e09b1
Method	BLASTX
NCBI GI	g3434975
BLAST score	392
E value	7.0e-38
Match length	172
% identity	54
NCBI Description	(AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
Seq. No.	8107
Contig ID	11571_2.R1040
5'-most EST	LIB3040-049-Q1-E1-E3
Method	BLASTX
NCBI GI	g3434975
BLAST score	210
E value	1.0e-16
Match length	141
% identity	44
NCBI Description	(AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

09684016-101000

5'-most EST gsv701047317.h1

Seq. No. 8127
 Contig ID 11641_1.R1040
 5'-most EST jC-gmf102220113h02a1
 Method BLASTX
 NCBI GI g4512708
 BLAST score 348
 E value 9.0e-33
 Match length 84
 % identity 76
 NCBI Description (AC006569) putative glutaredoxin [Arabidopsis thaliana]

Seq. No. 8128
 Contig ID 11641_2.R1040
 5'-most EST LIB3040-047-Q1-E1-H9
 Method BLASTX
 NCBI GI g4512708
 BLAST score 326
 E value 3.0e-30
 Match length 83
 % identity 75
 NCBI Description (AC006569) putative glutaredoxin [Arabidopsis thaliana]

Seq. No. 8129
 Contig ID 11656_1.R1040
 5'-most EST LIB3040-047-Q1-E1-F6
 Method BLASTX
 NCBI GI g4455325
 BLAST score 415
 E value 2.0e-40
 Match length 142
 % identity 56
 NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 8130
 Contig ID 11660_1.R1040
 5'-most EST LIB3051-031-Q1-K1-D8

Seq. No. 8131
 Contig ID 11660_3.R1040
 5'-most EST LIB3170-014-Q1-K1-C4

Seq. No. 8132
 Contig ID 11661_1.R1040
 5'-most EST LIB3040-047-Q1-E1-G12
 Method BLASTX
 NCBI GI g4490704
 BLAST score 548
 E value 6.0e-56
 Match length 215
 % identity 52
 NCBI Description (AL035680) putative protein [Arabidopsis thaliana]

Seq. No. 8133
 Contig ID 11668_1.R1040
 5'-most EST LIB3139-059-P1-N1-G6

Method BLASTX
 NCBI GI g2865175
 BLAST score 197
 E value 3.0e-15
 Match length 83
 % identity 48
 NCBI Description (AB010945) AtRer1A [Arabidopsis thaliana]

Seq. No. 8139
 Contig ID 11672_6.R1040
 5'-most EST rlr700897411.h1

Seq. No. 8140
 Contig ID 11673_1.R1040
 5'-most EST LIB3170-015-Q1-K1-C12

Seq. No. 8141
 Contig ID 11680_1.R1040
 5'-most EST LIB3072-023-Q1-E1-H11

Method BLASTX
 NCBI GI g1723738
 BLAST score 222
 E value 5.0e-18
 Match length 103
 % identity 30
 NCBI Description HYPOTHETICAL 55.1 KD PROTEIN IN TRX1-RTA1 INTERGENIC REGION
 >gi_2131699_pir_S64534 hypothetical protein YGR211w -
 yeast (Saccharomyces cerevisiae) >gi_1323379_emb_CAA97238
 (Z72996) ORF YGR211w [Saccharomyces cerevisiae] >gi_3510466
 (AF019769) zinc finger protein [Saccharomyces cerevisiae]

Seq. No. 8142
 Contig ID 11693_1.R1040
 5'-most EST LIB3040-047-Q1-E1-C4

Seq. No. 8143
 Contig ID 11693_2.R1040
 5'-most EST LIB3093-037-Q1-K1-G5

Seq. No. 8144
 Contig ID 11694_1.R1040
 5'-most EST ncj700979372.h1
 Method BLASTX
 NCBI GI g4455207
 BLAST score 443
 E value 7.0e-44
 Match length 91
 % identity 93
 NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 8145
 Contig ID 11695_1.R1040
 5'-most EST LIB3072-057-Q1-K1-G1
 Method BLASTX
 NCBI GI g1082054
 BLAST score 153
 E value 1.0e-09

09684016 101000

Match length	142
% identity	30
NCBI Description	(Z49859) copper transporter protein [Arabidopsis thaliana]
Seq. No.	8146
Contig ID	11695_2.R1040
5'-most EST	g4284406
Seq. No.	8147
Contig ID	11696_1.R1040
5'-most EST	LIB3040-047-Q1-E1-C7
Seq. No.	8148
Contig ID	11697_1.R1040
5'-most EST	LIB3170-085-Q1-J1-C2
Seq. No.	8149
Contig ID	11700_1.R1040
5'-most EST	LIB3050-015-Q1-E1-C4
Method	BLASTN
NCBI GI	g3449334
BLAST score	46
E value	1.0e-16
Match length	126
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.	8150
Contig ID	11707_1.R1040
5'-most EST	LIB3170-015-Q1-K1-C6
Seq. No.	8151
Contig ID	11708_1.R1040
5'-most EST	LIB3170-016-Q1-K1-C7
Seq. No.	8152
Contig ID	11712_1.R1040
5'-most EST	LIB3170-015-Q1-J1-C7
Method	BLASTX
NCBI GI	g4006878
BLAST score	140
E value	1.0e-08
Match length	47
% identity	53
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
Seq. No.	8153
Contig ID	11716_1.R1040
5'-most EST	LIB3040-046-Q1-E1-G9
Seq. No.	8154
Contig ID	11717_1.R1040
5'-most EST	LIB3040-047-Q1-E1-A7
Seq. No.	8155
Contig ID	11727_1.R1040

5'-most EST	LIB3040-046-Q1-E1-F9
Seq. No.	8156
Contig ID	11732_1.R1040
5'-most EST	LIB3170-016-Q1-K1-C2
Seq. No.	8157
Contig ID	11734_1.R1040
5'-most EST	LIB3170-015-Q1-K1-C2
Seq. No.	8158
Contig ID	11734_5.R1040
5'-most EST	leu701155165.h1
Seq. No.	8159
Contig ID	11734_8.R1040
5'-most EST	gsv701044315.h1
Seq. No.	8160
Contig ID	11737_1.R1040
5'-most EST	jC-gm1e01810092d05a1
Method	BLASTX
NCBI GI	g1699023
BLAST score	215
E value	9.0e-17
Match length	225
% identity	36
NCBI Description	(U78866) putative arginine-aspartate-rich RNA binding protein [Arabidopsis thaliana] >gi_1699051 (U78867) putative aspartate-arginine-rich mRNA binding protein [Arabidopsis thaliana]
Seq. No.	8161
Contig ID	11740_1.R1040
5'-most EST	gsv701044686.h1
Seq. No.	8162
Contig ID	11740_2.R1040
5'-most EST	LIB3170-013-Q1-K1-E2
Seq. No.	8163
Contig ID	11746_1.R1040
5'-most EST	LIB3109-001-Q1-K4-D1
Method	BLASTX
NCBI GI	g2760320
BLAST score	545
E value	2.0e-55
Match length	223
% identity	48
NCBI Description	(AC002130) F1N21.4 [Arabidopsis thaliana]
Seq. No.	8164
Contig ID	11755_1.R1040
5'-most EST	LIB3040-029-Q1-E1-E4
Method	BLASTN
NCBI GI	g3204128
BLAST score	200

Seq. No. 8170
 Contig ID 11763_1.R1040
 5'-most EST pmv700888903.h1
 Method BLASTX
 NCBI GI g3096931
 BLAST score 301
 E value 4.0e-27
 Match length 78
 % identity 71
 NCBI Description (AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]

Seq. No. 8171
 Contig ID 11768_1.R1040
 5'-most EST zzp700834271.h1

Seq. No. 8172
 Contig ID 11774_1.R1040
 5'-most EST LIB3040-046-Q1-E1-B12

Seq. No. 8173
 Contig ID 11785_1.R1040
 5'-most EST LIB3040-045-Q1-E1-G8

Seq. No. 8174
 Contig ID 11788_1.R1040
 5'-most EST LIB3040-045-Q1-E1-H12
 Method BLASTN
 NCBI GI g2244788
 BLAST score 56
 E value 1.0e-22
 Match length 197
 % identity 88
 NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 8175
 Contig ID 11788_2.R1040
 5'-most EST LIB3040-016-Q1-E1-G12
 Method BLASTN
 NCBI GI g2244788
 BLAST score 60
 E value 4.0e-25
 Match length 197
 % identity 89
 NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 8176
 Contig ID 11788_3.R1040
 5'-most EST zsg701127979.h1
 Method BLASTN
 NCBI GI g2244788
 BLAST score 47
 E value 2.0e-17
 Match length 133
 % identity 89

Seq. No. 8183
 Contig ID 11805_1.R1040
 5'-most EST LIB3106-043-Q1-K1-G7

Seq. No. 8184
 Contig ID 11807_1.R1040
 5'-most EST LIB3040-045-Q1-E1-F6
 Method BLASTN
 NCBI GI g1370179
 BLAST score 415
 E value 0.0e+00
 Match length 591
 % identity 93
 NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB5B

Seq. No. 8185
 Contig ID 11807_2.R1040
 5'-most EST uC-gmronoir038c03b1
 Method BLASTX
 NCBI GI g4559380
 BLAST score 315
 E value 3.0e-29
 Match length 89
 % identity 62
 NCBI Description (AC006526) putative auxin-responsive GH3 protein
 [Arabidopsis thaliana]

Seq. No. 8186
 Contig ID 11812_1.R1040
 5'-most EST LIB3040-045-Q1-E1-C2
 Method BLASTX
 NCBI GI g3249105
 BLAST score 424
 E value 3.0e-41
 Match length 188
 % identity 53
 NCBI Description (AC003114) Contains similarity to protein phosphatase 2C
 (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 8187
 Contig ID 11812_2.R1040
 5'-most EST LIB3109-017-Q1-K1-H8

Seq. No. 8188
 Contig ID 11818_1.R1040
 5'-most EST LIB3106-097-Q1-K1-E8

Seq. No. 8189
 Contig ID 11818_2.R1040
 5'-most EST kl1701214013.h1

Seq. No. 8190
 Contig ID 11819_1.R1040
 5'-most EST LIB3094-077-Q1-K1-D2

Seq. No. 8191

Contig ID 11821_1.R1040
 5'-most EST LIB3040-045-Q1-E1-D11
 Method BLASTN
 NCBI GI g470126
 BLAST score 36
 E value 1.0e-10
 Match length 121
 % identity 91
 NCBI Description N.tabacum (cv.Samsun NN) L19 mRNA for ribosomal protein L19

Seq. No. 8192
 Contig ID 11823_1.R1040
 5'-most EST LIB3170-068-Q1-J1-B9

Seq. No. 8193
 Contig ID 11837_1.R1040
 5'-most EST kmv700742945.h1
 Method BLASTX
 NCBI GI g3915196
 BLAST score 227
 E value 2.0e-23
 Match length 113
 % identity 51
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-C (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_1493838 (U52949) cyclin-specific ubiquitin carrier protein E2-C [Spisula solidissima]

Seq. No. 8194
 Contig ID 11847_1.R1040
 5'-most EST LIB3107-062-Q1-K1-G9
 Method BLASTN
 NCBI GI g11957
 BLAST score 80
 E value 9.0e-37
 Match length 120
 % identity 92
 NCBI Description Rice complete chloroplast genome

Seq. No. 8195
 Contig ID 11850_1.R1040
 5'-most EST LIB3040-044-Q1-E1-H4
 Method BLASTX
 NCBI GI g4115916
 BLAST score 191
 E value 2.0e-14
 Match length 84
 % identity 58
 NCBI Description (AF118222) F3H7.9 gene product [Arabidopsis thaliana] >gi_4539441_emb_CAB40029.1_ (AL049523) putative protein [Arabidopsis thaliana]

Seq. No. 8196
 Contig ID 11854_1.R1040
 5'-most EST jC-gmro02910016f04d1

Seq. No. 8197

Contig ID 11937_1.R1040
 5'-most EST taw700654539.h1
 Method BLASTX
 NCBI GI g4337206
 BLAST score 345
 E value 2.0e-32
 Match length 111
 % identity 61
 NCBI Description (AC006403) putative replication factor-A protein
 [Arabidopsis thaliana]

Seq. No. 8216
 Contig ID 11938_1.R1040
 5'-most EST jC-gmst02400062f11d1

Seq. No. 8217
 Contig ID 11940_1.R1040
 5'-most EST gsv701045940.h1
 Method BLASTX
 NCBI GI g1173074
 BLAST score 179
 E value 9.0e-13
 Match length 111
 % identity 37
 NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 (ALLERGEN CLA H 3) (CLA H
 III) >gi_1086177_pir_S41866 ribosomal P2 protein -
 Cladosporium herberum >gi_452606_emb_CAA54470_ (X77253)
 ribosomal P2 protein [Cladosporium herbarum]

Seq. No. 8218
 Contig ID 11952_1.R1040
 5'-most EST LIB3072-012-Q1-E1-C7

Seq. No. 8219
 Contig ID 11955_1.R1040
 5'-most EST sat701011736.h1
 Method BLASTX
 NCBI GI g2398521
 BLAST score 218
 E value 3.0e-22
 Match length 219
 % identity 42
 NCBI Description (Y13720) transcription factor [Arabidopsis thaliana]

Seq. No. 8220
 Contig ID 11955_2.R1040
 5'-most EST LIB3040-043-Q1-E1-B11

Seq. No. 8221
 Contig ID 11959_1.R1040
 5'-most EST rlr700900885.h1
 Method BLASTX
 NCBI GI g4115735
 BLAST score 257
 E value 5.0e-22
 Match length 131
 % identity 42

5'-most EST LIB3040-041-Q1-E1-H9
 Method BLASTX
 NCBI GI g1076414
 BLAST score 641
 E value 5.0e-67
 Match length 195
 % identity 64
 NCBI Description subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 8239
 Contig ID 12029_1.R1040
 5'-most EST gsv701046386.h1

Seq. No. 8240
 Contig ID 12031_1.R1040
 5'-most EST uC-gmflminsoy075g06b1
 Method BLASTX
 NCBI GI g2921873
 BLAST score 677
 E value 5.0e-71
 Match length 245
 % identity 52
 NCBI Description (AF047472) spleen mitotic checkpoint BUB3 [Homo sapiens] >gi_2981231_gb_AAC06258_ (AF053304) mitotic checkpoint component Bub3 [Homo sapiens] >gi_3639060 (AF081496) kinetochore protein BUB3 [Homo sapiens]

Seq. No. 8241
 Contig ID 12038_1.R1040
 5'-most EST leu701153034.h1
 Method BLASTX
 NCBI GI g4388731
 BLAST score 283
 E value 2.0e-25
 Match length 94
 % identity 64
 NCBI Description (AC006413) hypothetical protein [Arabidopsis thaliana]

Seq. No. 8242
 Contig ID 12041_1.R1040
 5'-most EST LIB3170-009-Q2-K1-H4

Seq. No. 8243
 Contig ID 12049_1.R1040
 5'-most EST LIB3040-016-Q1-E1-H2

Seq. No. 8244
 Contig ID 12049_2.R1040
 5'-most EST LIB3040-041-Q1-E1-G10

Seq. No. 8245
 Contig ID 12063_1.R1040
 5'-most EST LIB3040-041-Q1-E1-D7

Seq. No. 8246

Contig ID 12076 1.R1040
5'-most EST LIB3170-012-Q1-K1-H6

Seq. No. 8247
Contig ID 12080 1.R1040
5'-most EST LIB3051-029-Q1-K1-A1
Method BLASTX
NCBI GI g4544434
BLAST score 518
E value 2.0e-52
Match length 142
% identity 73
NCBI Description (AC006955) putative DNA-directed RNA polymerase II
[Arabidopsis thaliana]

Seq. No. 8248
Contig ID 12083 1.R1040
5'-most EST LIB3092-062-Q1-K1-C9
Method BLASTN
NCBI GI g4558521
BLAST score 44
E value 3.0e-15
Match length 152
% identity 82
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T10024,
complete sequence

Seq. No. 8249
Contig ID 12088 1.R1040
5'-most EST hrw701059278.h1

Seq. No. 8250
Contig ID 12096 1.R1040
5'-most EST LIB3040-040-Q1-E1-H8

Seq. No. 8251
Contig ID 12106 1.R1040
5'-most EST LIB3072-056-Q1-K1-E11
Method BLASTX
NCBI GI g4335723
BLAST score 273
E value 4.0e-24
Match length 79
% identity 61
NCBI Description (AC006248) putative thioredoxin M [Arabidopsis thaliana]

Seq. No. 8252
Contig ID 12115 1.R1040
5'-most EST LIB3170-009-Q2-K1-G10

Seq. No. 8253
Contig ID 12121 1.R1040
5'-most EST seb700651777.h1
Method BLASTX
NCBI GI g4115377
BLAST score 613
E value 1.0e-63

Seq. No. 8285
 Contig ID 12244_1.R1040
 5'-most EST uC-gmrominsoy097a11b1
 Method BLASTX
 NCBI GI g2190419
 BLAST score 480
 E value 5.0e-48
 Match length 150
 % identity 58
 NCBI Description (Y13632) dem [*Lycopersicon esculentum*]

Seq. No. 8286
 Contig ID 12255_1.R1040
 5'-most EST LIB3049-010-Q1-E1-D10
 Method BLASTN
 NCBI GI g4159703
 BLAST score 57
 E value 7.0e-23
 Match length 325
 % identity 85
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence [*Arabidopsis thaliana*]

Seq. No. 8287
 Contig ID 12255_2.R1040
 5'-most EST LIB3092-022-Q1-K1-C10
 Method BLASTN
 NCBI GI g4159703
 BLAST score 57
 E value 6.0e-23
 Match length 151
 % identity 90
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence [*Arabidopsis thaliana*]

Seq. No. 8288
 Contig ID 12255_3.R1040
 5'-most EST zhf700965132.h1
 Method BLASTX
 NCBI GI g2244797
 BLAST score 284
 E value 4.0e-25
 Match length 84
 % identity 65
 NCBI Description (Z97336) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 8289
 Contig ID 12255_4.R1040
 5'-most EST uC-gmropic006d07b1

Seq. No. 8290
 Contig ID 12255_5.R1040
 5'-most EST jC-gmle01810068b06a1

Seq. No. 8291
 Contig ID 12255_6.R1040

SECRET

NCBI GI g418507
 BLAST score 342
 E value 6.0e-32
 Match length 156
 % identity 46
 NCBI Description S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE
 METHYLTRANSFERASE >gi_541097_pir_S40872 hypothetical
 protein f161 - Escherichia coli >gi_305032 (L19201)
 ORF_f161 [Escherichia coli] >gi_1336002 (U56082)
 S-adenosylmethionine:2-demethylmenaquinone
 methyltransferase [Escherichia coli] >gi_1790364 (AE000467)
 menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No. 8300
 Contig ID 12277_2.R1040
 5'-most EST LIB3138-064-Q1-N1-B10
 Method BLASTX
 NCBI GI g418507
 BLAST score 165
 E value 2.0e-11
 Match length 53
 % identity 58
 NCBI Description S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE
 METHYLTRANSFERASE >gi_541097_pir_S40872 hypothetical
 protein f161 - Escherichia coli >gi_305032 (L19201)
 ORF_f161 [Escherichia coli] >gi_1336002 (U56082)
 S-adenosylmethionine:2-demethylmenaquinone
 methyltransferase [Escherichia coli] >gi_1790364 (AE000467)
 menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No. 8301
 Contig ID 12279_1.R1040
 5'-most EST LIB3087-012-Q1-K1-E5
 Method BLASTX
 NCBI GI g2160182
 BLAST score 293
 E value 4.0e-26
 Match length 155
 % identity 44
 NCBI Description (AC000132) ESTs gb_ATTS1236, gb_T43334, gb_N97019, gb_AA395203
 come from this gene. [Arabidopsis thaliana]

Seq. No. 8302
 Contig ID 12279_2.R1040
 5'-most EST LIB3107-057-Q1-K1-F1

Seq. No. 8303
 Contig ID 12282_1.R1040
 5'-most EST LIB3074-011-Q1-E1-H7
 Method BLASTX
 NCBI GI g466160
 BLAST score 372
 E value 2.0e-35
 Match length 83
 % identity 86
 NCBI Description HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
 >gi_630771_pir_S44903 ZK652.3 protein - Caenorhabditis

0967019-1

0967019-1000

0967019-1

0967019-1000

0967019-1000

0967019-1

NCBI Description (AE000725) argininosuccinate synthase [Aquifex aeolicus]

Seq. No. 8342
Contig ID 12383_4.R1040
5'-most EST gsv701044237.h1

Seq. No. 8343
Contig ID 12387_1.R1040
5'-most EST LIB3139-048-P1-N1-A2
Method BLASTN
NCBI GI g1694899
BLAST score 391
E value 0.0e+00
Match length 583
% identity 92
NCBI Description P.sativum mRNA for Cop1 protein

Seq. No. 8344
Contig ID 12388_1.R1040
5'-most EST g5057689
Method BLASTX
NCBI GI g3193320
BLAST score 154
E value 7.0e-10
Match length 78
% identity 38
NCBI Description (AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana]

Seq. No. 8345
Contig ID 12391_1.R1040
5'-most EST LIB3170-010-Q1-J1-E7

Seq. No. 8346
Contig ID 12393_1.R1040
5'-most EST zhf700963357.h1

Seq. No. 8347
Contig ID 12395_1.R1040
5'-most EST LIB3040-036-Q1-E1-E11

Seq. No. 8348
Contig ID 12406_1.R1040
5'-most EST LIB3040-036-Q1-E1-B10

Seq. No. 8349
Contig ID 12407_1.R1040
5'-most EST LIB3040-036-Q1-E1-B11
Method BLASTX
NCBI GI g2245118
BLAST score 695
E value 5.0e-73
Match length 153
% identity 79
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

13.6 kDa subunit [Arabidopsis thaliana]

Seq. No. 8356
 Contig ID 12438_3.R1040
 5'-most EST LIB3050-013-Q1-E1-H7
 Method BLASTX
 NCBI GI g3219858
 BLAST score 403
 E value 2.0e-39
 Match length 91
 % identity 84
 NCBI Description DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE
 >gi_2129724_pir_S71204 RNA polymerase II 13.6 kDa chain -
 Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II
 13.6 kDa subunit [Arabidopsis thaliana]

Seq. No. 8357
 Contig ID 12438_4.R1040
 5'-most EST bth700844772.h1
 Method BLASTX
 NCBI GI g3219858
 BLAST score 169
 E value 3.0e-12
 Match length 44
 % identity 73
 NCBI Description DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE
 >gi_2129724_pir_S71204 RNA polymerase II 13.6 kDa chain -
 Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II
 13.6 kDa subunit [Arabidopsis thaliana]

Seq. No. 8358
 Contig ID 12439_1.R1040
 5'-most EST LIB3170-012-Q1-K1-E6

Seq. No. 8359
 Contig ID 12443_1.R1040
 5'-most EST LIB3170-011-Q1-K1-E7

Seq. No. 8360
 Contig ID 12446_1.R1040
 5'-most EST fua701040824.h1
 Method BLASTX
 NCBI GI g1834379
 BLAST score 183
 E value 3.0e-13
 Match length 98
 % identity 43
 NCBI Description (Y10551) ComAB [Bacillus licheniformis]

Seq. No. 8361
 Contig ID 12452_1.R1040
 5'-most EST zpv700763308.h1
 Method BLASTN
 NCBI GI g4103986
 BLAST score 109
 E value 6.0e-54
 Match length 282

Seq. No. 8369
Contig ID 12483_1.R1040
5'-most EST LIB3040-035-Q1-E1-A1

Seq. No. 8370
Contig ID 12484_1.R1040
5'-most EST LIB3040-034-Q1-E1-G2

Seq. No. 8371
Contig ID 12490_1.R1040
5'-most EST LIB3170-010-Q1-K1-D2

Seq. No. 8372
Contig ID 12493_1.R1040
5'-most EST jC-gmle01810063h01a1
Method BLASTX
NCBI GI g2894599
BLAST score 258
E value 4.0e-22
Match length 71
% identity 53
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 8373
Contig ID 12493_2.R1040
5'-most EST jC-gmle01810010e01a1
Method BLASTX
NCBI GI g2894599
BLAST score 296
E value 1.0e-26
Match length 100
% identity 56
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 8374
Contig ID 12493_3.R1040
5'-most EST bth700848738.h1
Method BLASTX
NCBI GI g2894599
BLAST score 531
E value 6.0e-57
Match length 195
% identity 64
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 8375
Contig ID 12493_5.R1040
5'-most EST LIB3138-033-Q1-N1-A4
Method BLASTX
NCBI GI g2894599
BLAST score 252
E value 1.0e-21
Match length 100
% identity 53
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 8376


```
Contig ID      12500_1.R1040
5'-most EST   LIB3094-091-Q1-K1-E7
Method        BLASTX
NCBI GI       g3759184
BLAST score    1082
E value       1.0e-118
Match length   290
% identity     70
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
```

```
Seq. No.          8377
Contig ID         12500_2.R1040
5'-most EST      zsg701122572.h1
Method            BLASTX
NCBI GI           g3759184
BLAST score       336
E value           2.0e-31
Match length      109
% identity        61
NCBI Description  (AB018441) phi-1 [Nicotiana tabacum]
```

```
Seq. No.          8378
Contig ID         12500_3.R1040
5'-most EST      LIB3139-084-P1-N1-G3
Method            BLASTX
NCBI GI           g3759184
BLAST score       504
E value           6.0e-51
Match length      163
% identity        60
NCBI Description  (AB018441) phi-1 [Nicotiana tabacum]
```

```
Seq. No.          8379
Contig ID         12500_6.R1040
5'-most EST      rlr700898648.h1
Method            BLASTX
NCBI GI           g3759184
BLAST score       164
E value           3.0e-11
Match length      40
% identity        78
NCBI Description  (AB018441) phi-1 [Nicotiana tabacum]
```

Seq. No.	8380
Contig ID	12500_7.R1040
5'-most EST	LIB3139-056-P1-N1-G1
Method	BLASTX
NCBI GI	g4325369
BLAST score	248
E value	7.0e-31
Match length	107
% identity	63
NCBI Description	(AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No.	8381
Contig ID	12508_1.R1040
5'-most EST	LIB3040-034-Q1-E1-G11

0954016 101000

0954016 101000

0954016 101000

0954016 101000

0954016 101000

0954016 101000

0954016 101000

0954016 101000

Match length	146
% identity	85
NCBI Description	Arabidopsis thaliana 20S proteasome subunit PAF1 (PAF1) mRNA, complete cds
Seq. No.	8398
Contig ID	12553_1.R1040
5'-most EST	LIB3073-023-Q1-K1-A7
Method	BLASTX
NCBI GI	g3914555
BLAST score	337
E value	1.0e-31
Match length	86
% identity	85
NCBI Description	PUTATIVE RIBOSOME-BINDING FACTOR A, CHLOROPLAST PRECURSOR >gi_3096942_emb_CAA18852.1_ (AL023094) putative protein [Arabidopsis thaliana]
Seq. No.	8399
Contig ID	12555_1.R1040
5'-most EST	LIB3040-033-Q1-E1-F3
Method	BLASTX
NCBI GI	g4262232
BLAST score	532
E value	5.0e-54
Match length	212
% identity	48
NCBI Description	(AC006200) putative ribosomal protein L7 [Arabidopsis thaliana]
Seq. No.	8400
Contig ID	12555_3.R1040
5'-most EST	LIB3049-026-Q1-E1-G7
Seq. No.	8401
Contig ID	12555_4.R1040
5'-most EST	fua701042636.h1
Seq. No.	8402
Contig ID	12561_1.R1040
5'-most EST	LIB3040-033-Q1-E1-G12
Seq. No.	8403
Contig ID	12565_1.R1040
5'-most EST	LIB3139-045-P1-N1-A6
Seq. No.	8404
Contig ID	12576_1.R1040
5'-most EST	sat701014478.h1
Method	BLASTN
NCBI GI	g2502084
BLAST score	219
E value	1.0e-119
Match length	431
% identity	88
NCBI Description	Vigna radiata adenosine triphosphatase mRNA, partial cds

Seq. No. 8412
Contig ID 12590_5.R1040
5'-most EST zpv700758707.h1

Seq. No. 8413
Contig ID 12604_1.R1040
5'-most EST LIB3170-009-Q2-J1-D6

Seq. No. 8414
Contig ID 12608_1.R1040
5'-most EST LIB3170-011-Q1-J1-C9

Seq. No. 8415
Contig ID 12609_1.R1040
5'-most EST bth700849741.h1

Seq. No. 8416
Contig ID 12613_1.R1040
5'-most EST vwf700674168.h1

Seq. No. 8417
Contig ID 12613_2.R1040
5'-most EST vwf700673719.h1

Seq. No. 8418
Contig ID 12618_1.R1040
5'-most EST LIB3040-032-Q1-E1-F6

Seq. No. 8419
Contig ID 12621_1.R1040
5'-most EST LIB3040-032-Q1-E1-D8

Seq. No. 8420
Contig ID 12633_1.R1040
5'-most EST LIB3040-032-Q1-E1-F4

Seq. No. 8421
Contig ID 12648_1.R1040
5'-most EST LIB3040-020-Q1-E1-B5
Method BLASTX
NCBI GI g2914702
BLAST score 322
E value 2.0e-29
Match length 222
% identity 50
NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

Seq. No. 8422
Contig ID 12652_1.R1040
5'-most EST LIB3051-048-Q1-K1-D8

Seq. No. 8423
Contig ID 12671_1.R1040
5'-most EST LIB3170-012-Q1-K1-C1

Seq. No. 8424

Contig ID 12716_1.R1040
 5'-most EST uaw700664678.h1
 Method BLASTX
 NCBI GI g4468991
 BLAST score 183
 E value 2.0e-13
 Match length 104
 % identity 39
 NCBI Description (AL035605) ribosomal-like protein [Arabidopsis thaliana]

Seq. No. 8438
 Contig ID 12723_1.R1040
 5'-most EST LIB3040-031-Q1-E1-H4
 Method BLASTN
 NCBI GI g971167
 BLAST score 114
 E value 3.0e-57
 Match length 254
 % identity 86
 NCBI Description Pisum sativum Wando ornithine carbamoyltransferase mRNA, complete cds

Seq. No. 8439
 Contig ID 12728_1.R1040
 5'-most EST ssr700556271.h1
 Method BLASTX
 NCBI GI g4455213
 BLAST score 1168
 E value 1.0e-128
 Match length 258
 % identity 84
 NCBI Description (AL035440) glutamine amidotransferase/cyclase [Arabidopsis thaliana]

Seq. No. 8440
 Contig ID 12730_1.R1040
 5'-most EST LIB3040-031-Q1-E2-A7
 Method BLASTX
 NCBI GI g4455293
 BLAST score 267
 E value 3.0e-23
 Match length 61
 % identity 87
 NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 8441
 Contig ID 12730_2.R1040
 5'-most EST kl1701213870.h1

Seq. No. 8442
 Contig ID 12750_1.R1040
 5'-most EST LIB3049-055-Q1-E1-F3
 Method BLASTN
 NCBI GI g488564
 BLAST score 170
 E value 1.0e-90
 Match length 410

% identity 86
NCBI Description Medicago sativa cultivar Chief histone H3.1 gene, 5' region and complete cds

Seq. No. 8443
Contig ID 12752_1.R1040
5'-most EST epX701104867.h1

Seq. No. 8444
Contig ID 12752_2.R1040
5'-most EST LIB3050-025-Q1-K1-D2

Seq. No. 8445
Contig ID 12752_3.R1040
5'-most EST LIB3093-037-Q1-K1-B6

Seq. No. 8446
Contig ID 12759_1.R1040
5'-most EST LIB3040-031-Q1-E1-C9

Seq. No. 8447
Contig ID 12769_1.R1040
5'-most EST LIB3040-030-Q1-E1-G5
Method BLASTX
NCBI GI g2829751
BLAST score 206
E value 5.0e-16
Match length 114
% identity 38
NCBI Description MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF)
>gi_1850559 (U88035) macrophage migration inhibitory factor [Brugia malayi] >gi_2190976 (AF002699) macrophage migration inhibitory factor [Brugia malayi]

Seq. No. 8448
Contig ID 12774_1.R1040
5'-most EST LIB3040-030-Q1-E1-H1

Seq. No. 8449
Contig ID 12784_1.R1040
5'-most EST LIB3049-034-Q1-E1-E12

Seq. No. 8450
Contig ID 12789_1.R1040
5'-most EST leu701149449.h1
Method BLASTX
NCBI GI g1718097
BLAST score 1090
E value 1.0e-119
Match length 340
% identity 58
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir_A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

09634016.101000

Seq. No. 8451
 Contig ID 12793_1.R1040
 5'-most EST bth700843731.h1
 Method BLASTX
 NCBI GI g3763916
 BLAST score 377
 E value 8.0e-36
 Match length 260
 % identity 33
 NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]
 >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown
 protein [Arabidopsis thaliana]

Seq. No. 8452
 Contig ID 12796_1.R1040
 5'-most EST zzp700832237.h1
 Method BLASTX
 NCBI GI g4468813
 BLAST score 387
 E value 3.0e-37
 Match length 202
 % identity 39
 NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 8453
 Contig ID 12796_2.R1040
 5'-most EST LIB3139-121-P1-N1-G4

Seq. No. 8454
 Contig ID 12796_3.R1040
 5'-most EST gsv701045344.h1

Seq. No. 8455
 Contig ID 12802_1.R1040
 5'-most EST LIB3040-030-Q1-E1-C5

Seq. No. 8456
 Contig ID 12802_2.R1040
 5'-most EST leu701145651.h1

Seq. No. 8457
 Contig ID 12802_4.R1040
 5'-most EST LIB3040-005-Q1-E1-A1

Seq. No. 8458
 Contig ID 12808_1.R1040
 5'-most EST asn701135489.h1

Seq. No. 8459
 Contig ID 12810_1.R1040
 5'-most EST LIB3170-012-Q1-K1-B10

Seq. No. 8460
 Contig ID 12815_1.R1040
 5'-most EST ncj700977424.h1
 Method BLASTX
 NCBI GI g2731377

BLAST score 253
 E value 1.0e-21
 Match length 143
 % identity 38
 NCBI Description (U28739) similar to alcohol dehydrogenase/ribitol dehydrogenase [Caenorhabditis elegans]

Seq. No. 8461
 Contig ID 12817_1.R1040
 5'-most EST LIB3040-030-Q1-E1-A3
 Method BLASTN
 NCBI GI g2695738
 BLAST score 56
 E value 9.0e-23
 Match length 68
 % identity 96
 NCBI Description Pisum sativum mitochondrial tRNA-Gly gene and flanking sequences

Seq. No. 8462
 Contig ID 12819_1.R1040
 5'-most EST ncj700975520.h1

Seq. No. 8463
 Contig ID 12820_1.R1040
 5'-most EST LIB3170-012-Q1-K1-B4

Seq. No. 8464
 Contig ID 12831_1.R1040
 5'-most EST uC-gmrominsoy316e04b1
 Method BLASTX
 NCBI GI g4544409
 BLAST score 1156
 E value 1.0e-127
 Match length 376
 % identity 60
 NCBI Description (AC006955) putative transcription factor [Arabidopsis thaliana]

Seq. No. 8465
 Contig ID 12831_2.R1040
 5'-most EST uC-gmrominsoy180c03b1
 Method BLASTX
 NCBI GI g4544409
 BLAST score 194
 E value 2.0e-14
 Match length 69
 % identity 59
 NCBI Description (AC006955) putative transcription factor [Arabidopsis thaliana]

Seq. No. 8466
 Contig ID 12831_3.R1040
 5'-most EST LIB3051-072-Q1-K1-E10
 Method BLASTX
 NCBI GI g2244917
 BLAST score 285

09684016-101000

E value 5.0e-25
Match length 139
% identity 45
NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 8467
Contig ID 12831_4.R1040
5'-most EST LIB3093-034-Q1-K1-D7

Seq. No. 8468
Contig ID 12831_5.R1040
5'-most EST uC-gmropic042d01b1

Seq. No. 8469
Contig ID 12831_6.R1040
5'-most EST LIB3092-008-Q1-K1-F1
Method BLASTX
NCBI GI g2244917
BLAST score 161
E value 1.0e-10
Match length 65
% identity 46
NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 8470
Contig ID 12831_7.R1040
5'-most EST jex700905749.h1

Seq. No. 8471
Contig ID 12840_1.R1040
5'-most EST LIB3109-029-Q1-K1-G1
Method BLASTX
NCBI GI g3122357
BLAST score 370
E value 2.0e-35
Match length 98
% identity 70
NCBI Description PUTATIVE LIPOATE-PROTEIN LIGASE B (LIPOATE BIOSYNTHESIS PROTEIN B) >gi_2494127 (AC002376) Contains similarity to Mycobacterium LIPB gene (gb_Q104041). [Arabidopsis thaliana]

Seq. No. 8472
Contig ID 12856_1.R1040
5'-most EST LIB3106-069-P1-K1-F8

Seq. No. 8473
Contig ID 12867_1.R1040
5'-most EST LIB3051-006-Q1-K1-A11

Seq. No. 8474
Contig ID 12872_1.R1040
5'-most EST LIB3093-016-Q1-K1-F11
Method BLASTX
NCBI GI g1665817
BLAST score 200
E value 2.0e-15

Match length 128
 % identity 36
 NCBI Description (D87466) Similar to S.cerevisiae hypothetical protein L3111 (S59316) [Homo sapiens]

Seq. No. 8475
 Contig ID 12873_1.R1040
 5'-most EST LIB3170-010-Q1-K1-A6

Seq. No. 8476
 Contig ID 12873_2.R1040
 5'-most EST LIB3170-006-Q1-K1-C10

Seq. No. 8477
 Contig ID 12875_1.R1040
 5'-most EST LIB3170-011-Q1-K1-A5

Seq. No. 8478
 Contig ID 12882_1.R1040
 5'-most EST LIB3040-029-Q1-E1-B3

Seq. No. 8479
 Contig ID 12883_1.R1040
 5'-most EST LIB3040-020-Q1-E1-B11
 Method BLASTX
 NCBI GI g4559346
 BLAST score 407
 E value 1.0e-39
 Match length 122
 % identity 61
 NCBI Description (AC006585) early nodulin 16 [Arabidopsis thaliana]

Seq. No. 8480
 Contig ID 12883_2.R1040
 5'-most EST hrw701062307.h1

Seq. No. 8481
 Contig ID 12884_1.R1040
 5'-most EST kmv700741435.h1

Seq. No. 8482
 Contig ID 12898_1.R1040
 5'-most EST LIB3170-011-Q1-J1-A4

Seq. No. 8483
 Contig ID 12905_1.R1040
 5'-most EST uC-gmropic016c07b1
 Method BLASTX
 NCBI GI g3355468
 BLAST score 526
 E value 2.0e-53
 Match length 123
 % identity 88
 NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No. 8484

Seq. No. 8489
 Contig ID 12920_1.R1040
 5'-most EST LIB3040-008-Q1-E1-B4
 Method BLASTX
 NCBI GI g2443886
 BLAST score 314
 E value 1.0e-28
 Match length 87
 % identity 76
 NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No. 8490
 Contig ID 12920_2.R1040
 5'-most EST zhf700961575.h1

Seq. No. 8491
 Contig ID 12920_5.R1040
 5'-most EST zhf700964127.h1

Seq. No. 8492
 Contig ID 12943_1.R1040
 5'-most EST LIB3040-026-Q1-E1-D12
 Method BLASTX
 NCBI GI g2832625
 BLAST score 759
 E value 9.0e-81
 Match length 221
 % identity 66
 NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 8493
 Contig ID 12959_1.R1040
 5'-most EST LIB3040-027-Q1-E1-G10

Seq. No. 8494
 Contig ID 12965_1.R1040
 5'-most EST LIB3040-027-Q1-E1-G6
 Method BLASTX
 NCBI GI g2326363
 BLAST score 301
 E value 7.0e-36
 Match length 121
 % identity 65
 NCBI Description (AJ001037) DNA-directed RNA polymerase [Arabidopsis thaliana]

Seq. No. 8495
 Contig ID 12970_1.R1040
 5'-most EST LIB3040-027-Q1-E1-H2

Seq. No. 8496
 Contig ID 12976_1.R1040
 5'-most EST uaw700664514.h1
 Method BLASTN
 NCBI GI g2760166
 BLAST score 40


```

% identity          91
NCBI Description    (AC006528) putative DNA replication licensing factor with
                    an MCM family domain (prosite:PDOC00662) [Arabidopsis
                    thaliana]

Seq. No.           8509
Contig ID          13033_1.R1040
5'-most EST        LIB3093-037-Q1-K1-F12
Method             BLASTX
NCBI GI            g2826786
BLAST score        301
E value            4.0e-27
Match length       123
% identity         54
NCBI Description    (Y10905) RAPB protein [Oryza sativa]

Seq. No.           8510
Contig ID          13033_3.R1040
5'-most EST        bth700849432.h1

Seq. No.           8511
Contig ID          13034_1.R1040
5'-most EST        LIB3170-007-Q1-K1-G12

Seq. No.           8512
Contig ID          13036_1.R1040
5'-most EST        LIB3170-005-Q1-K1-G3
Method             BLASTX
NCBI GI            g3582021
BLAST score        473
E value            2.0e-47
Match length       149
% identity         60
NCBI Description    (Y09423) cytochrome P450 [Nepeta racemosa]

Seq. No.           8513
Contig ID          13041_1.R1040
5'-most EST        LIB3040-026-Q1-E1-D2
Method             BLASTX
NCBI GI            g3935184
BLAST score        194
E value            8.0e-15
Match length       93
% identity         49
NCBI Description    (AC004557) F17L21.27 [Arabidopsis thaliana]

Seq. No.           8514
Contig ID          13045_1.R1040
5'-most EST        jC-gm1e01810094d11a1
Method             BLASTX
NCBI GI            g3021285
BLAST score        250
E value            2.0e-21
Match length       75
% identity         65
NCBI Description    (AL022347) hypothetical protein [Arabidopsis thaliana]
>gi_3451058_emb_CAA20454.1_ (AL031326) hypothetical protein

```


Method BLASTX
 NCBI GI g464981
 BLAST score 752
 E value 5.0e-80
 Match length 147
 % identity 93
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
 LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)
 ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 8536
 Contig ID 13115_1.R1040
 5'-most EST leu701157895.h1
 Method BLASTX
 NCBI GI g4490308
 BLAST score 1004
 E value 1.0e-109
 Match length 303
 % identity 67
 NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 8537
 Contig ID 13116_1.R1040
 5'-most EST bth700848141.h1
 Method BLASTX
 NCBI GI g3687243
 BLAST score 256
 E value 7.0e-22
 Match length 67
 % identity 76
 NCBI Description (AC005169) putative ribosomal protein [Arabidopsis
 thaliana]

Seq. No. 8538
 Contig ID 13116_2.R1040
 5'-most EST pmv700888753.h1
 Method BLASTX
 NCBI GI g3687243
 BLAST score 254
 E value 9.0e-22
 Match length 66
 % identity 74
 NCBI Description (AC005169) putative ribosomal protein [Arabidopsis
 thaliana]

Seq. No. 8539
 Contig ID 13121_1.R1040
 5'-most EST uC-gmflminsoy008b03b1

Seq. No. 8540
 Contig ID 13124_1.R1040
 5'-most EST LIB3170-007-Q1-K1-F9

Seq. No. 8541
 Contig ID 13128_1.R1040
 5'-most EST LIB3170-006-Q1-K1-F1

Seq. No. 8542
 Contig ID 13130_1.R1040
 5'-most EST zsg701123209.h1
 Method BLASTX
 NCBI GI g2559012
 BLAST score 375
 E value 1.0e-35
 Match length 128
 % identity 58
 NCBI Description (AF026293) chaperonin containing t-complex polypeptide 1, beta subunit; CCT-beta [Homo sapiens] >gi_4090929
 (AF026166) chaperonin-containing TCP-1 beta subunit homolog [Homo sapiens]

Seq. No. 8543
 Contig ID 13133_1.R1040
 5'-most EST LIB3170-007-Q1-K1-F12

Seq. No. 8544
 Contig ID 13134_1.R1040
 5'-most EST leu701144349.h1
 Method BLASTN
 NCBI GI g4388705
 BLAST score 37
 E value 4.0e-11
 Match length 142
 % identity 89
 NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 8545
 Contig ID 13134_3.R1040
 5'-most EST LIB3138-013-Q1-N1-G2
 Method BLASTX
 NCBI GI g4115731
 BLAST score 160
 E value 7.0e-11
 Match length 86
 % identity 44
 NCBI Description (AB017507) Apg12 [Homo sapiens]

Seq. No. 8546
 Contig ID 13137_1.R1040
 5'-most EST LIB3040-025-Q1-E1-C11

Seq. No. 8547
 Contig ID 13137_2.R1040
 5'-most EST epx701105423.h1

Seq. No. 8548
 Contig ID 13140_1.R1040
 5'-most EST LIB3092-053-Q1-K1-D9

Seq. No. 8549
 Contig ID 13147_1.R1040
 5'-most EST g5676941

Seq. No. 8550
 Contig ID 13147 2.R1040
 5'-most EST LIB3074-025-Q1-E1-D1
 Method BLASTN
 NCBI GI g728715
 BLAST score 75
 E value 7.0e-34
 Match length 191
 % identity 85
 NCBI Description S.oleracea mRNA for 6.1 kDa polypeptide of photosystem II

Seq. No. 8551
 Contig ID 13147 4.R1040
 5'-most EST LIB3074-028-Q1-K1-A9
 Method BLASTX
 NCBI GI g2493694
 BLAST score 180
 E value 4.0e-13
 Match length 98
 % identity 42
 NCBI Description PHOTOSYSTEM II REACTION CENTRE W PROTEIN PRECURSOR (PSII 6.1 KD PROTEIN) >gi_1076268_pir_S53025 photosystem II protein - spinach >gi_728716_emb_CAA59409_ (X85038) protein of photosystem II [Spinacia oleracea]

Seq. No. 8552
 Contig ID 13149 1.R1040
 5'-most EST LIB3170-007-Q1-K1-F3
 Method BLASTX
 NCBI GI g3328587
 BLAST score 334
 E value 1.0e-33
 Match length 165
 % identity 50
 NCBI Description (AE001292) CMP-2-keto-3-deoxyoctulosonic acid synthetase [Chlamydia trachomatis]

Seq. No. 8553
 Contig ID 13151 1.R1040
 5'-most EST LIB3040-024-Q1-E1-G5

Seq. No. 8554
 Contig ID 13158 1.R1040
 5'-most EST LIB3138-015-Q1-N2-E2

Seq. No. 8555
 Contig ID 13158 2.R1040
 5'-most EST uC-gmflminsoy043f05b1

Seq. No. 8556
 Contig ID 13158 3.R1040
 5'-most EST leu701154395.h1

Seq. No. 8557
 Contig ID 13159 1.R1040
 5'-most EST uC-gmropic041a09b1

Seq. No. 8563
 Contig ID 13173_1.R1040
 5'-most EST LIB3051-027-Q1-K1-G8
 Method BLASTX
 NCBI GI g4056425
 BLAST score 744
 E value 9.0e-79
 Match length 164
 % identity 82
 NCBI Description (AC005322) ESTs gb_H36249, gb_AA59732 and gb_AA651219 come from this gene. [Arabidopsis thaliana]

Seq. No. 8564
 Contig ID 13173_2.R1040
 5'-most EST LIB3170-006-Q1-K1-E8

Seq. No. 8565
 Contig ID 13178_1.R1040
 5'-most EST LIB3072-051-Q1-E1-C1
 Method BLASTN
 NCBI GI g2764803
 BLAST score 146
 E value 2.0e-76
 Match length 366
 % identity 85
 NCBI Description G.max mRNA for epoxide hydrolase

Seq. No. 8566
 Contig ID 13182_1.R1040
 5'-most EST LIB3040-023-Q1-E1-G8
 Method BLASTX
 NCBI GI g3702329
 BLAST score 156
 E value 2.0e-10
 Match length 50
 % identity 62
 NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 8567
 Contig ID 13183_1.R1040
 5'-most EST hrw701056967.h1
 Method BLASTX
 NCBI GI g2811026
 BLAST score 357
 E value 9.0e-34
 Match length 80
 % identity 88
 NCBI Description TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi_1946375 (U93215)
 TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana]
 >gi_2347204 (AC002338) TCP1-chaperonin cofactor A isolog
 [Arabidopsis thaliana]

Seq. No. 8568
 Contig ID 13183_2.R1040
 5'-most EST LIB3040-023-Q1-E1-G9
 Method BLASTX
 NCBI GI g2811026

09684016-101000

Contig ID 13235 1.R1040
 5'-most EST LIB3040-022-Q1-E1-H5
 Method BLASTX
 NCBI GI g2232057
 BLAST score 232
 E value 5.0e-19
 Match length 69
 % identity 67
 NCBI Description (AF000177) CaSm [Homo sapiens]

Seq. No. 8580
 Contig ID 13235 2.R1040
 5'-most EST jex700905452.h1

Seq. No. 8581
 Contig ID 13242 1.R1040
 5'-most EST LIB3049-052-Q1-E1-G2

Seq. No. 8582
 Contig ID 13244 1.R1040
 5'-most EST LIB3170-004-Q1-K1-A10
 Method BLASTX
 NCBI GI g4490737
 BLAST score 509
 E value 2.0e-51
 Match length 184
 % identity 34
 NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 8583
 Contig ID 13256 1.R1040
 5'-most EST LIB3040-022-Q1-E1-G3

Seq. No. 8584
 Contig ID 13260 1.R1040
 5'-most EST epx701105025.h1

Seq. No. 8585
 Contig ID 13266 1.R1040
 5'-most EST wrq700786736.h2

Seq. No. 8586
 Contig ID 13270 1.R1040
 5'-most EST LIB3170-005-Q1-K1-H4

Seq. No. 8587
 Contig ID 13274 1.R1040
 5'-most EST LIB3170-006-Q1-J1-E6

Seq. No. 8588
 Contig ID 13285 1.R1040
 5'-most EST LIB3040-022-Q1-E1-A10

Seq. No. 8589
 Contig ID 13288 1.R1040
 5'-most EST LIB3040-022-Q1-E1-A6
 Method BLASTX

09684015.101000

NCBI GI g3132470
BLAST score 179
E value 5.0e-13
Match length 96
% identity 50
NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]

Seq. No. 8596
Contig ID 13304_2.R1040
5'-most EST uC-gmflminsoy084b04b1

Seq. No. 8597
Contig ID 13308_1.R1040
5'-most EST hrw701060302.h1
Method BLASTX
NCBI GI g2739376
BLAST score 263
E value 8.0e-23
Match length 90
% identity 58
NCBI Description (AC002505) putative permease [Arabidopsis thaliana]

Seq. No. 8598
Contig ID 13316_1.R1040
5'-most EST kl1701208551.h1
Method BLASTX
NCBI GI g2132842
BLAST score 344
E value 4.0e-32
Match length 118
% identity 53
NCBI Description probable membrane protein YOL077c - yeast (Saccharomyces cerevisiae) >gi_1419909_emb_CAA99087_ (Z74819) ORF YOL077c [Saccharomyces cerevisiae]

Seq. No. 8599
Contig ID 13323_1.R1040
5'-most EST hrw701060978.h1

Seq. No. 8600
Contig ID 13324_1.R1040
5'-most EST LIB3040-021-Q1-E1-D4

Seq. No. 8601
Contig ID 13335_1.R1040
5'-most EST LIB3170-007-Q1-K1-C5
Method BLASTX
NCBI GI g499693
BLAST score 491
E value 2.0e-49
Match length 167
% identity 65
NCBI Description (L32095) cyclophilin [Vicia faba]

Seq. No. 8602
Contig ID 13337_1.R1040
5'-most EST LIB3040-021-Q1-E1-A4

Seq. No. 8603
 Contig ID 13339_1.R1040
 5'-most EST LIB3170-006-Q1-K1-C1
 Method BLASTX
 NCBI GI g2344897
 BLAST score 150
 E value 1.0e-09
 Match length 100
 % identity 43
 NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 8604
 Contig ID 13342_1.R1040
 5'-most EST rlr700897809.h1
 Method BLASTX
 NCBI GI g4158232
 BLAST score 548
 E value 4.0e-56
 Match length 110
 % identity 88
 NCBI Description (Y18626) reversibly glycosylated polypeptide [Triticum aestivum]

Seq. No. 8605
 Contig ID 13345_1.R1040
 5'-most EST LIB3040-021-Q1-E1-C12
 Method BLASTX
 NCBI GI g2739371
 BLAST score 293
 E value 2.0e-26
 Match length 68
 % identity 84
 NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 8606
 Contig ID 13364_1.R1040
 5'-most EST uC-gmflminsoy036f09b1
 Method BLASTX
 NCBI GI g2244834
 BLAST score 186
 E value 1.0e-13
 Match length 96
 % identity 53
 NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 8607
 Contig ID 13381_1.R1040
 5'-most EST LIB3040-020-Q1-E1-E1

Seq. No. 8608
 Contig ID 13385_1.R1040
 5'-most EST LIB3040-020-Q1-E1-C6
 Method BLASTX
 NCBI GI g4263701
 BLAST score 335
 E value 3.0e-31

09684015-101000

Match length 110
 % identity 64
 NCBI Description (AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No. 8609
 Contig ID 13388_1.R1040
 5'-most EST LIB3049-028-Q1-E1-G3
 Method BLASTX
 NCBI GI g3650030
 BLAST score 255
 E value 1.0e-21
 Match length 78
 % identity 59
 NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]

Seq. No. 8610
 Contig ID 13396_1.R1040
 5'-most EST LIB3040-020-Q1-E1-D8

Seq. No. 8611
 Contig ID 13415_1.R1040
 5'-most EST LIB3040-020-Q1-E1-C1

Seq. No. 8612
 Contig ID 13416_1.R1040
 5'-most EST LIB3040-019-Q1-E1-F7
 Method BLASTX
 NCBI GI g4249662
 BLAST score 275
 E value 2.0e-46
 Match length 118
 % identity 84
 NCBI Description (AF089810) Altered Response to Gravity [Arabidopsis thaliana]

Seq. No. 8613
 Contig ID 13421_1.R1040
 5'-most EST LIB3040-019-Q1-E1-G11

Seq. No. 8614
 Contig ID 13422_1.R1040
 5'-most EST LIB3106-111-Q1-K1-F11
 Method BLASTX
 NCBI GI g132918
 BLAST score 334
 E value 5.0e-31
 Match length 75
 % identity 87

NCBI Description 50S RIBOSOMAL PROTEIN L35, CHLOROPLAST PRECURSOR (CL35)
 >gi_81486_pir_A36107 ribosomal protein L35 precursor,
 chloroplast - spinach >gi_170139 (M60449) ribosomal protein
 L35 [Spinacia oleracea]

Seq. No. 8615
 Contig ID 13422_2.R1040
 5'-most EST LIB3040-011-Q1-E1-B5
 Method BLASTX

NCBI GI g132918
 BLAST score 314
 E value 1.0e-28
 Match length 102
 % identity 73
 NCBI Description 50S RIBOSOMAL PROTEIN L35, CHLOROPLAST PRECURSOR (CL35)
 >gi_81486_pir_A36107 ribosomal protein L35 precursor,
 chloroplast - spinach >gi_170139 (M60449) ribosomal protein
 L35 [Spinacia oleracea]

Seq. No. 8616
 Contig ID 13426_1.R1040
 5'-most EST LIB3109-018-Q1-K1-A4

Seq. No. 8617
 Contig ID 13427_1.R1040
 5'-most EST LIB3073-021-Q1-K1-C1

Seq. No. 8618
 Contig ID 13433_1.R1040
 5'-most EST bth700848210.h1
 Method BLASTX
 NCBI GI g2144099
 BLAST score 188
 E value 3.0e-14
 Match length 77
 % identity 42
 NCBI Description Set alpha isoform - rat >gi_545263_bbs_143660 (S68589) Set
 alpha isoform=leukemogenesis protein {alternatively
 spliced} [rats, neonatal kidney, Peptide, 289 aa] [Rattus
 sp.] >gi_741750_prf_2008109A set gene [Rattus norvegicus]

Seq. No. 8619
 Contig ID 13439_1.R1040
 5'-most EST LIB3073-003-Q1-K1-F3
 Method BLASTX
 NCBI GI g585960
 BLAST score 206
 E value 4.0e-16
 Match length 42
 % identity 93
 NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT
 >gi_433665_emb_CAA81412_ (Z26753) Sec61 beta-subunit
 homolog [Arabidopsis thaliana]

Seq. No. 8620
 Contig ID 13442_1.R1040
 5'-most EST zzp700836203.h1
 Method BLASTX
 NCBI GI g3885334
 BLAST score 182
 E value 2.0e-13
 Match length 48
 % identity 65
 NCBI Description (AC005623) putative argonaute protein [Arabidopsis
 thaliana]

Seq. No. 8629
 Contig ID 13489_1.R1040
 5'-most EST LIB3051-117-Q1-K1-F11
 Method BLASTX
 NCBI GI g1705678
 BLAST score 1079
 E value 1.0e-161
 Match length 312
 % identity 72
 NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
 valosin-containing protein [Glycine max]

Seq. No. 8630
 Contig ID 13490_1.R1040
 5'-most EST gsv701054670.h1

Seq. No. 8631
 Contig ID 13495_1.R1040
 5'-most EST LIB3040-018-Q1-E1-E5
 Method BLASTX
 NCBI GI g3805765
 BLAST score 224
 E value 3.0e-18
 Match length 54
 % identity 76
 NCBI Description (AC005693) putative protein kinase [Arabidopsis thaliana]

Seq. No. 8632
 Contig ID 13498_1.R1040
 5'-most EST smc700750158.h1
 Method BLASTX
 NCBI GI g2501538
 BLAST score 153
 E value 6.0e-10
 Match length 91
 % identity 40
 NCBI Description HYPOTHETICAL 51.0 KD PROTEIN SLL0996
 >gi_1652230_dbj_BAA17153_ (D90904) hypothetical protein
 [Synechocystis sp.]

Seq. No. 8633
 Contig ID 13500_1.R1040
 5'-most EST LIB3040-018-Q1-E1-C4

Seq. No. 8634
 Contig ID 13501_1.R1040
 5'-most EST LIB3040-018-Q1-E1-C6
 Method BLASTX
 NCBI GI g3122853
 BLAST score 383
 E value 1.0e-36
 Match length 250
 % identity 25
 NCBI Description WD-REPEAT PROTEIN SAZD >gi_1082863_pir_A49367 transducin homolog sazD - human >gi_414536 (U02609) transducin-like protein [Homo sapiens]

09684015-101000

BLAST score 786
E value 6.0e-84
Match length 228
% identity 73
NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No. 8647
Contig ID 13551_1.R1040
5'-most EST LIB3170-061-Q1-J1-E1
Method BLASTN
NCBI GI g3599418
BLAST score 63
E value 1.0e-26
Match length 80
% identity 95
NCBI Description Glycine max alternative oxidase precursor (Aox1) gene,
nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 8648
Contig ID 13558_1.R1040
5'-most EST zsg701124685.h1
Method BLASTX
NCBI GI g4580466
BLAST score 372
E value 2.0e-35
Match length 100
% identity 74
NCBI Description (AC006081) putative 50S ribosomal protein L4 [Arabidopsis
thaliana]

Seq. No. 8649
Contig ID 13558_2.R1040
5'-most EST LIB3040-017-Q1-E1-F2

Seq. No. 8650
Contig ID 13575_1.R1040
5'-most EST LIB3040-017-Q1-E1-D2

Seq. No. 8651
Contig ID 13577_1.R1040
5'-most EST LIB3040-017-Q1-E1-D7

Seq. No. 8652
Contig ID 13579_1.R1040
5'-most EST LIB3040-017-Q1-E1-C12
Method BLASTX
NCBI GI g3201610
BLAST score 323
E value 5.0e-30
Match length 70
% identity 77
NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]

Seq. No. 8653
Contig ID 13583_1.R1040
5'-most EST LIB3170-002-Q1-K1-H8
Method BLASTX

Contig ID 13674 1.R1040
 5'-most EST uaw700663720.h1
 Method BLASTX
 NCBI GI g544150
 BLAST score 106
 E value 1.0e-10
 Match length 157
 % identity 32
 NCBI Description DEK PROTEIN >gi_284375_pir_S26059 probable transforming protein (dek) - human >gi_30503_emb_CAA45536_ (X64229) putative oncogene [Homo sapiens] >gi_4007163_emb_CAA21138_ (AL031774) dek (putative oncogene) [Homo sapiens] >gi_4503249_ref_NP_003463.1_pD6S231E_ DEK gene

Seq. No. 8675
 Contig ID 13674 2.R1040
 5'-most EST jC-gmle01810030d12d1

Seq. No. 8676
 Contig ID 13676 1.R1040
 5'-most EST LIB3040-015-Q1-E1-D10
 Method BLASTN
 NCBI GI g2924257
 BLAST score 92
 E value 3.0e-44
 Match length 222
 % identity 85
 NCBI Description Tobacco chloroplast genome DNA

Seq. No. 8677
 Contig ID 13681 1.R1040
 5'-most EST LIB3040-015-Q1-E1-D6

Seq. No. 8678
 Contig ID 13684 1.R1040
 5'-most EST LIB3040-015-Q1-E1-D9

Seq. No. 8679
 Contig ID 13686 1.R1040
 5'-most EST LIB3040-015-Q1-E1-E10
 Method BLASTX
 NCBI GI g2392769
 BLAST score 281
 E value 7.0e-25
 Match length 94
 % identity 60
 NCBI Description (AC002534) putative histone deacetylase [Arabidopsis thaliana]

Seq. No. 8680
 Contig ID 13687 1.R1040
 5'-most EST zhf700960830.h1
 Method BLASTX
 NCBI GI g3341685
 BLAST score 403
 E value 4.0e-39
 Match length 134

% identity 64
 NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 8681
 Contig ID 13720_1.R1040
 5'-most EST LIB3170-002-Q1-K1-G6

Seq. No. 8682
 Contig ID 13724_1.R1040
 5'-most EST gsv701047493.h1
 Method BLASTX
 NCBI GI g170753
 BLAST score 753
 E value 7.0e-80
 Match length 185
 % identity 74
 NCBI Description (M95819) initiation factor (iso)4F p28 subunit [Triticum aestivum]

Seq. No. 8683
 Contig ID 13730_1.R1040
 5'-most EST LIB3049-002-Q1-E1-F10
 Method BLASTX
 NCBI GI g2262102
 BLAST score 255
 E value 2.0e-21
 Match length 202
 % identity 39
 NCBI Description (AC002343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 8684
 Contig ID 13734_1.R1040
 5'-most EST LIB3051-109-Q1-K1-G3
 Method BLASTX
 NCBI GI g1174779
 BLAST score 1918
 E value 0.0e+00
 Match length 449
 % identity 83
 NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi_166894 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana] >gi_4490703_emb_CAB38837.1 (AL035680) tryptophan synthase beta-subunit (TSB2) [Arabidopsis thaliana]

Seq. No. 8685
 Contig ID 13734_2.R1040
 5'-most EST ssr700560895.h1
 Method BLASTX
 NCBI GI g1174779
 BLAST score 200
 E value 8.0e-16
 Match length 72
 % identity 60
 NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi_166894 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana] >gi_4490703_emb_CAB38837.1 (AL035680) tryptophan synthase beta-subunit (TSB2) [Arabidopsis thaliana]

Contig ID 13858_1.R1040
 5'-most EST LIB3040-012-Q1-E1-F5
 Method BLASTX
 NCBI GI g3142294
 BLAST score 1676
 E value 0.0e+00
 Match length 374
 % identity 91
 NCBI Description (AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from *S. pombe*. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [*Arabidopsis thaliana*]

Seq. No. 8717
 Contig ID 13858_2.R1040
 5'-most EST kl1701205184.h1
 Method BLASTX
 NCBI GI g2832707
 BLAST score 227
 E value 8.0e-19
 Match length 56
 % identity 84
 NCBI Description (AL021713) translation initiation factor eIF-2 gamma chain-like protein [*Arabidopsis thaliana*]

Seq. No. 8718
 Contig ID 13863_1.R1040
 5'-most EST uC-gmflminsoy003c10b1
 Method BLASTX
 NCBI GI g4008441
 BLAST score 458
 E value 2.0e-45
 Match length 143
 % identity 62
 NCBI Description (AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [*Caenorhabditis elegans*]

Seq. No. 8719
 Contig ID 13863_2.R1040
 5'-most EST ckk700605883.h2
 Method BLASTX
 NCBI GI g4008441
 BLAST score 212
 E value 5.0e-28
 Match length 100
 % identity 65
 NCBI Description (AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [*Caenorhabditis elegans*]

Seq. No. 8720
 Contig ID 13863_3.R1040
 5'-most EST LIB3051-002-Q1-E1-F4
 Method BLASTX
 NCBI GI g4008441

09684016 "101000

E value 1.0e-24
Match length 107
% identity 61
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 8729
Contig ID 13889_1.R1040
5'-most EST LIB3170-004-Q1-K1-F1

Seq. No. 8730
Contig ID 13891_1.R1040
5'-most EST LIB3040-011-Q1-E1-H5
Method BLASTX
NCBI GI g2245124
BLAST score 734
E value 1.0e-77
Match length 241
% identity 65
NCBI Description (Z97343) protein kinase [Arabidopsis thaliana]

Seq. No. 8731
Contig ID 13891_3.R1040
5'-most EST uC-gmflminsoy008c09b1
Method BLASTX
NCBI GI g2245124
BLAST score 167
E value 1.0e-11
Match length 74
% identity 53
NCBI Description (Z97343) protein kinase [Arabidopsis thaliana]

Seq. No. 8732
Contig ID 13900_1.R1040
5'-most EST fde700876566.h1
Method BLASTX
NCBI GI g4522012
BLAST score 706
E value 2.0e-74
Match length 234
% identity 58
NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 8733
Contig ID 13902_1.R1040
5'-most EST LIB3170-002-Q1-K1-E3

Seq. No. 8734
Contig ID 13903_1.R1040
5'-most EST LIB3170-001-Q1-K1-E4

Seq. No. 8735
Contig ID 13906_1.R1040
5'-most EST asn701134208.h1
Method BLASTX
NCBI GI g349379
BLAST score 342
E value 3.0e-39

0001016 101000

5'-most EST LIB3170-003-Q1-J1-E2
 Method BLASTN
 NCBI GI g3599418
 BLAST score 104
 E value 7.0e-52
 Match length 135
 % identity 94
 NCBI Description Glycine max alternative oxidase precursor (Aox1) gene,
 nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 8752
 Contig ID 14001_1.R1040
 5'-most EST LIB3094-062-Q1-K1-C7
 Method BLASTN
 NCBI GI g2062691
 BLAST score 34
 E value 3.0e-09
 Match length 34
 % identity 62
 NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete
 cds

Seq. No. 8753
 Contig ID 14001_2.R1040
 5'-most EST LIB3040-010-Q1-E1-A10

Seq. No. 8754
 Contig ID 14004_1.R1040
 5'-most EST LIB3170-001-Q1-J1-D4

Seq. No. 8755
 Contig ID 14013_1.R1040
 5'-most EST LIB3049-039-Q1-E1-D11

Seq. No. 8756
 Contig ID 14047_1.R1040
 5'-most EST LIB3050-024-Q1-K1-C5
 Method BLASTX
 NCBI GI g3236242
 BLAST score 428
 E value 6.0e-42
 Match length 103
 % identity 84
 NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis
 thaliana]

Seq. No. 8757
 Contig ID 14047_2.R1040
 5'-most EST LIB3093-027-Q1-K1-H11
 Method BLASTX
 NCBI GI g3236242
 BLAST score 407
 E value 1.0e-39
 Match length 99
 % identity 83
 NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis
 thaliana]

Seq. No. 8758
 Contig ID 14047_3.R1040
 5'-most EST LIB3049-049-Q1-E1-E6
 Method BLASTX
 NCBI GI g1710546
 BLAST score 437
 E value 4.0e-43
 Match length 106
 % identity 79
 NCBI Description 60S RIBOSOMAL PROTEIN L36 >gi_1276967 (U47095) putative ribosomal protein [Daucus carota]

Seq. No. 8759
 Contig ID 14047_4.R1040
 5'-most EST vwf700675179.h1
 Method BLASTX
 NCBI GI g1710546
 BLAST score 346
 E value 6.0e-33
 Match length 75
 % identity 89
 NCBI Description 60S RIBOSOMAL PROTEIN L36 >gi_1276967 (U47095) putative ribosomal protein [Daucus carota]

Seq. No. 8760
 Contig ID 14049_1.R1040
 5'-most EST LIB3040-009-Q1-E1-B11

Seq. No. 8761
 Contig ID 14057_1.R1040
 5'-most EST LIB3040-009-Q1-E1-C5

Seq. No. 8762
 Contig ID 14058_1.R1040
 5'-most EST eep700870490.h1
 Method BLASTX
 NCBI GI g1532168
 BLAST score 251
 E value 2.0e-21
 Match length 66
 % identity 73
 NCBI Description (U63815) localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initiation codon and stop codon could not be precisely determined [Arabidopsis thaliana]

Seq. No. 8763
 Contig ID 14066_1.R1040
 5'-most EST LIB3170-006-Q1-K1-H7
 Method BLASTX
 NCBI GI g2829910
 BLAST score 440
 E value 2.0e-43
 Match length 234
 % identity 45

E value 5.0e-15
 Match length 53
 % identity 60
 NCBI Description (Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST yk375c3.3 comes from this gene [Caenorhabditis elegans]

Seq. No. 8771
 Contig ID 14092_1.R1040
 5'-most EST LIB3170-039-Q1-K2-F2
 Method BLASTX
 NCBI GI g2924520
 BLAST score 754
 E value 6.0e-80
 Match length 273
 % identity 82
 NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No. 8772
 Contig ID 14096_1.R1040
 5'-most EST LIB3106-067-P1-K1-C6
 Method BLASTX
 NCBI GI g2618688
 BLAST score 430
 E value 2.0e-42
 Match length 99
 % identity 77
 NCBI Description (AC002510) putative esterase D [Arabidopsis thaliana]

Seq. No. 8773
 Contig ID 14104_1.R1040
 5'-most EST gsv701049590.h1
 Method BLASTX
 NCBI GI g2194132
 BLAST score 485
 E value 7.0e-49
 Match length 156
 % identity 59
 NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]

Seq. No. 8774
 Contig ID 14105_1.R1040
 5'-most EST pxt700945486.h1
 Method BLASTX
 NCBI GI g4314389
 BLAST score 326
 E value 3.0e-30
 Match length 91
 % identity 68
 NCBI Description (AC006232) putative transcription factor [Arabidopsis thaliana]

Seq. No. 8775
 Contig ID 14114_1.R1040
 5'-most EST LIB3170-002-Q1-K1-C4

Seq. No. 8776

Contig ID	14116_1.R1040
5'-most EST	LIB3051-067-Q1-K1-B5
Method	BLASTN
NCBI GI	g2351065
BLAST score	43
E value	1.0e-14
Match length	130
% identity	74
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]
Seq. No.	8777
Contig ID	14120_1.R1040
5'-most EST	LIB3107-017-Q1-K1-C12
Seq. No.	8778
Contig ID	14120_2.R1040
5'-most EST	g4307297
Method	BLASTX
NCBI GI	g1938549
BLAST score	203
E value	1.0e-15
Match length	122
% identity	42
NCBI Description	(U97016) similar to drosophila Rlcl gene product (NID:g563361) and S. cerevisiae mitochondrial 60S ribosomal protein L4 (YML4) (NID:g459259) [Caenorhabditis elegans]
Seq. No.	8779
Contig ID	14122_1.R1040
5'-most EST	jC-gmro02910011b12a1
Method	BLASTX
NCBI GI	g2583120
BLAST score	262
E value	2.0e-40
Match length	143
% identity	47
NCBI Description	(AC002387) putative receptor-like protein kinase [Arabidopsis thaliana]
Seq. No.	8780
Contig ID	14128_1.R1040
5'-most EST	LIB3049-032-Q1-E1-D9
Seq. No.	8781
Contig ID	14137_1.R1040
5'-most EST	LIB3040-008-Q1-E1-A2
Seq. No.	8782
Contig ID	14137_2.R1040
5'-most EST	LIB3106-105-Q1-K1-E2
Seq. No.	8783
Contig ID	14146_1.R1040
5'-most EST	LIB3049-025-Q1-E1-B1
Method	BLASTX
NCBI GI	g3184100

BLAST score 270
 E value 2.0e-23
 Match length 72
 % identity 67
 NCBI Description (AL023777) rna binding protein [Schizosaccharomyces pombe]

Seq. No. 8784
 Contig ID 14146_2.R1040
 5'-most EST asn701142530.h1

Seq. No. 8785
 Contig ID 14164_1.R1040
 5'-most EST LIB3040-007-Q1-E1-A8
 Method BLASTX
 NCBI GI g3269289
 BLAST score 371
 E value 2.0e-35
 Match length 112
 % identity 66
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 8786
 Contig ID 14164_2.R1040
 5'-most EST zsg701123057.h1
 Method BLASTX
 NCBI GI g3269289
 BLAST score 369
 E value 3.0e-35
 Match length 137
 % identity 69
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 8787
 Contig ID 14174_1.R1040
 5'-most EST LIB3073-026-Q1-K1-G11

Seq. No. 8788
 Contig ID 14174_2.R1040
 5'-most EST LIB3170-004-Q1-K1-C1

Seq. No. 8789
 Contig ID 14176_1.R1040
 5'-most EST LIB3170-003-Q1-K1-C1

Seq. No. 8790
 Contig ID 14204_1.R1040
 5'-most EST zpv700760194.h1
 Method BLASTX
 NCBI GI g3367536
 BLAST score 521
 E value 7.0e-53
 Match length 117
 % identity 88
 NCBI Description (AC004392) Contains similarity to symbiosis-related like protein FlN20.80 gi_2961343 from A. thaliana BAC gb_AL022140. EST gb_T04695 comes from this gene. [Arabidopsis thaliana]

5'-most EST pmv700889748.h1
 Method BLASTX
 NCBI GI g4455754
 BLAST score 164
 E value 6.0e-11
 Match length 160
 % identity 28
 NCBI Description (AL035478) hypothetical protein SC2G5.30 [Streptomyces coelicolor]

Seq. No. 8804
 Contig ID 14242_1.R1040
 5'-most EST jC-gmro02910025g01d1
 Method BLASTX
 NCBI GI g4220485
 BLAST score 455
 E value 4.0e-45
 Match length 139
 % identity 64
 NCBI Description (AC006069) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No. 8805
 Contig ID 14245_1.R1040
 5'-most EST LIB3170-002-Q1-K1-A11

Seq. No. 8806
 Contig ID 14251_1.R1040
 5'-most EST jC-gmst02400071e04a1
 Method BLASTX
 NCBI GI g4006827
 BLAST score 686
 E value 2.0e-72
 Match length 182
 % identity 71
 NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 8807
 Contig ID 14252_1.R1040
 5'-most EST LIB3051-037-Q1-K1-C6
 Method BLASTN
 NCBI GI g3821780
 BLAST score 37
 E value 5.0e-11
 Match length 37
 % identity 100
 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 8808
 Contig ID 14252_2.R1040
 5'-most EST LIB3040-005-Q1-E1-F9

Seq. No. 8809
 Contig ID 14282_1.R1040
 5'-most EST LIB3040-005-Q1-E1-A12

Seq. No. 8810

0967016-10000

5'-most EST LIB3107-034-Q1-K1-H6

Seq. No. 8822
Contig ID 14326_5.R1040
5'-most EST sat701010945.h1

Seq. No. 8823
Contig ID 14342_1.R1040
5'-most EST jC-gmst02400042h11a1
Method BLASTX
NCBI GI g2388913
BLAST score 141
E value 1.0e-08
Match length 104
% identity 42
NCBI Description (Z98974) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 8824
Contig ID 14344_1.R1040
5'-most EST LIB3170-020-Q1-J1-G12

Seq. No. 8825
Contig ID 14351_1.R1040
5'-most EST uC-gmropic083h01b1
Method BLASTX
NCBI GI g4544453
BLAST score 376
E value 4.0e-36
Match length 105
% identity 73
NCBI Description (AC006592) hypothetical protein [Arabidopsis thaliana]

Seq. No. 8826
Contig ID 14351_2.R1040
5'-most EST LIB3170-019-Q1-K1-G10
Method BLASTX
NCBI GI g4544453
BLAST score 280
E value 1.0e-31
Match length 89
% identity 81
NCBI Description (AC006592) hypothetical protein [Arabidopsis thaliana]

Seq. No. 8827
Contig ID 14357_1.R1040
5'-most EST k11701209107.h1
Method BLASTX
NCBI GI g4521249
BLAST score 468
E value 2.0e-46
Match length 268
% identity 46
NCBI Description (AB013912) DNA helicase [Mus musculus]

Seq. No. 8828
Contig ID 14358_1.R1040
5'-most EST LIB3040-004-Q1-E1-A1

Seq. No. 8829
 Contig ID 14359_1.R1040
 5'-most EST LIB3040-004-Q1-E1-A11
 Method BLASTX
 NCBI GI g3980034
 BLAST score 286
 E value 2.0e-25
 Match length 81
 % identity 65
 NCBI Description (AL033514) predicted using Genefinder; cDNA EST EMBL:D71127 comes from this gene; cDNA EST EMBL:D73731 comes from this gene [Caenorhabditis elegans]

Seq. No. 8830
 Contig ID 14362_1.R1040
 5'-most EST zhf700959092.h1

Seq. No. 8831
 Contig ID 14377_1.R1040
 5'-most EST uC-gmrominsoy203b10b1
 Method BLASTX
 NCBI GI g4455224
 BLAST score 357
 E value 2.0e-37
 Match length 188
 % identity 46
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 8832
 Contig ID 14382_1.R1040
 5'-most EST LIB3040-003-Q1-E1-G4

Seq. No. 8833
 Contig ID 14386_1.R1040
 5'-most EST ncj700985656.h1
 Method BLASTX
 NCBI GI g2257503
 BLAST score 437
 E value 8.0e-43
 Match length 272
 % identity 38
 NCBI Description (AB004535) BEM46 PROTEIN [Schizosaccharomyces pombe]

Seq. No. 8834
 Contig ID 14386_2.R1040
 5'-most EST kl1701213588.h1

Seq. No. 8835
 Contig ID 14387_1.R1040
 5'-most EST LIB3040-003-Q1-E1-D1

Seq. No. 8836
 Contig ID 14398_1.R1040
 5'-most EST LIB3170-079-Q1-J1-G1

Seq. No. 8837

BLAST score 244
 E value 7.0e-25
 Match length 96
 % identity 62
 NCBI Description (AF128395) contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]

Seq. No. 8847
 Contig ID 14434_1.R1040
 5'-most EST LIB3040-002-Q1-E1-E7

Seq. No. 8848
 Contig ID 14437_1.R1040
 5'-most EST LIB3170-020-Q1-J1-F8

Seq. No. 8849
 Contig ID 14447_1.R1040
 5'-most EST LIB3040-002-Q1-E1-G11

Seq. No. 8850
 Contig ID 14450_1.R1040
 5'-most EST LIB3040-002-Q1-E1-C6
 Method BLASTX
 NCBI GI g2947062
 BLAST score 248
 E value 7.0e-21
 Match length 168
 % identity 42
 NCBI Description (AC002521) unknown protein [Arabidopsis thaliana]

Seq. No. 8851
 Contig ID 14457_1.R1040
 5'-most EST LIB3170-079-Q1-K1-D10
 Method BLASTX
 NCBI GI g2134723
 BLAST score 275
 E value 1.0e-23
 Match length 191
 % identity 38
 NCBI Description AlkB homolog protein ABH - human >gi_1237210_emb_CAA63047_ (X91992) alkB homolog protein [Homo sapiens]
 >gi_1588535_prf__2208455A ABH gene [Homo sapiens]

Seq. No. 8852
 Contig ID 14458_1.R1040
 5'-most EST LIB3040-002-Q1-E1-D8
 Method BLASTX
 NCBI GI g466044
 BLAST score 153
 E value 3.0e-15
 Match length 146
 % identity 35
 NCBI Description HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III
 >gi_630780_pir_S44909 ZK686.4 protein - Caenorhabditis elegans >gi_304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis]

00000000000000000000

Seq. No.	8854
Contig ID	14463_3.R1040
5'-most EST	leu701144523.h1

Seq. No.	8856
Contig ID	14469_1.R1040
5'-most EST	jC-gmRo02910034b12a1
Method	BLASTN
NCBI GI	g3819163
BLAST score	586
E value	0.0e+00
Match length	638
% identity	98
NCBI Description	Glycine max cctd gene

Seq. No.	8858
Contig ID	14481_1.R1040
5'-most EST	rlr700901879.h1

```
Seq. No.      8860
Contig ID     14483_1.R1040
5'-most EST   jC-gmfl02220077f06a1
Method        BLASTX
```


BLAST score	103
E value	1.0e-09
Match length	119
% identity	34
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
Seq. No.	8929
Contig ID	14808_1.R1040
5'-most EST	LIB3170-039-Q1-K2-H2
Method	BLASTX
NCBI GI	g4544386
BLAST score	685
E value	3.0e-72
Match length	157
% identity	79
NCBI Description	(AC007047) putative cell division control protein [Arabidopsis thaliana]
Seq. No.	8930
Contig ID	14809_2.R1040
5'-most EST	zhf700961825.h1
Method	BLASTX
NCBI GI	g3047104
BLAST score	565
E value	3.0e-58
Match length	157
% identity	70
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	8931
Contig ID	14810_1.R1040
5'-most EST	LIB3049-055-Q1-E1-E5
Seq. No.	8932
Contig ID	14818_1.R1040
5'-most EST	LIB3049-055-Q1-E1-F4
Seq. No.	8933
Contig ID	14820_1.R1040
5'-most EST	ssr700555180.h1
Seq. No.	8934
Contig ID	14821_1.R1040
5'-most EST	LIB3049-055-Q1-E1-F7
Method	BLASTX
NCBI GI	g3915463
BLAST score	225
E value	5.0e-23
Match length	136
% identity	46
NCBI Description	HYPOTHETICAL 33.1 KD PROTEIN SLR1592 >gi_1652063_dbj_BAA16988_ (D90902) hypothetical protein [Synechocystis sp.]
Seq. No.	8935
Contig ID	14822_1.R1040

[illegible]

Seq. No.	8937
Contig ID	14829_1.R1040
5'-most EST	leu701148315.h1

```
Seq. No.      8939
Contig ID     14832_1.R1040
5'-most EST   LIB3049-012-Q1-E1-D1
Method        BLASTX
NCBI GI       g3297808
BLAST score    248
E value       4.0e-21
Match length   97
% identity     52
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
```

Seq. No.	8941
Contig ID	14847_1.R1040
5'-most EST	LIB3049-055-Q1-E1-B3

Seq. No.	8943
Contig ID	14850_1.R1040
5'-most EST	LIB3170-037-Q1-K1-H2

Method BLASTX
 NCBI GI g4455800
 BLAST score 404
 E value 8.0e-39
 Match length 145
 % identity 55
 NCBI Description (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No. 8951
 Contig ID 14865_2.R1040
 5'-most EST jC-gmro02800031g07a1
 Method BLASTX
 NCBI GI g1729891
 BLAST score 184
 E value 1.0e-13
 Match length 108
 % identity 35
 NCBI Description TEGT PROTEIN (TESTIS ENHANCED GENE TRANSCRIPT)
 >gi_2136254_pir_I38334 TEGT (testis enhanced gene
 transcript) - human >gi_458545_emb_CAA53472_(X75861) TEGT
 [Homo sapiens] >gi_4507433_ref_NP_003208.1_pTEGT_testis
 enhanced gene transcript

Seq. No. 8952
 Contig ID 14869_1.R1040
 5'-most EST LIB3049-055-Q1-E1-A11

Seq. No. 8953
 Contig ID 14869_2.R1040
 5'-most EST LIB3109-018-Q1-K1-A8
 Method BLASTX
 NCBI GI g3047102
 BLAST score 187
 E value 5.0e-14
 Match length 86
 % identity 43
 NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 8954
 Contig ID 14872_1.R1040
 5'-most EST g5126928

Seq. No. 8955
 Contig ID 14873_1.R1040
 5'-most EST jC-gmf102220097c01a1
 Method BLASTN
 NCBI GI g2275194
 BLAST score 226
 E value 1.0e-124
 Match length 662
 % identity 84
 NCBI Description Arabidopsis thaliana chromosome II BAC T08I13 genomic
 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 8956
 Contig ID 14882_1.R1040
 5'-most EST LIB3051-058-Q1-K2-F4

Method	BLASTX
NCBI GI	g2708624
BLAST score	1543
E value	1.0e-172
Match length	358
% identity	76
NCBI Description	(AF036618) acetyl-CoA synthetase [Arabidopsis thaliana]
Seq. No.	8957
Contig ID	14888_1.R1040
5'-most EST	LIB3170-039-Q1-K2-E1
Method	BLASTX
NCBI GI	g2160173
BLAST score	179
E value	5.0e-13
Match length	78
% identity	46
NCBI Description	(AC000132) Similar to N. tabacum salt-inducible protein (gb_U08285). [Arabidopsis thaliana]
Seq. No.	8958
Contig ID	14891_1.R1040
5'-most EST	jC-gmst02400073a05a1
Method	BLASTX
NCBI GI	g4432823
BLAST score	433
E value	2.0e-42
Match length	240
% identity	45
NCBI Description	(AC006593) hypothetical protein [Arabidopsis thaliana]
Seq. No.	8959
Contig ID	14910_1.R1040
5'-most EST	k11701205175.h1
Method	BLASTX
NCBI GI	g1172874
BLAST score	210
E value	2.0e-16
Match length	149
% identity	43
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi_479589_pir_S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf_1913421A rd22 gene [Arabidopsis thaliana]
Seq. No.	8960
Contig ID	14912_2.R1040
5'-most EST	LIB3049-054-Q1-E1-B7
Method	BLASTX
NCBI GI	g2252838
BLAST score	159
E value	2.0e-10
Match length	155
% identity	27
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs
gb_H36782 and gb_F14074 come from this gene. [Arabidopsis
thaliana]

Seq. No. 8966
Contig ID 14926_1.R1040
5'-most EST ssr700555756.h1

Seq. No. 8967
Contig ID 14926_2.R1040
5'-most EST uC-gmflminsoy078f07b1

Seq. No. 8968
Contig ID 14926_3.R1040
5'-most EST LIB3170-035-Q1-K1-F10

Seq. No. 8969
Contig ID 14931_1.R1040
5'-most EST LIB3049-046-Q1-E1-H4

Seq. No. 8970
Contig ID 14932_1.R1040
5'-most EST LIB3170-033-Q1-K1-F12

Seq. No. 8971
Contig ID 14945_1.R1040
5'-most EST LIB3170-034-Q1-K1-H2
Method BLASTN
NCBI GI g1420886
BLAST score 124
E value 5.0e-63
Match length 302
% identity 86
NCBI Description Phaseolus vulgaris non-specific lipid transfer-like protein
mRNA, complete cds

Seq. No. 8972
Contig ID 14947_1.R1040
5'-most EST LIB3093-038-Q1-K1-A6
Method BLASTX
NCBI GI g1352267
BLAST score 405
E value 2.0e-39
Match length 147
% identity 56
NCBI Description DEOXYHYPUSINE SYNTHASE >gi_994715 (L39068) deoxyhypusine
synthase [Homo sapiens] >gi_1710220 (U79262) deoxyhypusine
synthase [Homo sapiens] >gi_3021398_emb_CAA04940_
(AJ001701) deoxyhypusine synthase [Homo sapiens]
>gi_4503325_ref_NP_001921.1_pDHPS_ deoxyhypusine synthase

Seq. No. 8973
Contig ID 14948_1.R1040
5'-most EST trc700567438.h1

Seq. No. 8974
Contig ID 14949_1.R1040

Method	BLASTX
NCBI GI	g3785997
BLAST score	622
E value	9.0e-65
Match length	200
% identity	62
NCBI Description	(AC005499) putative annexin [Arabidopsis thaliana]
Seq. No.	9002
Contig ID	15000_1.R1040
5'-most EST	uC-gmronoir053e10b1
Seq. No.	9003
Contig ID	15000_2.R1040
5'-most EST	dpv701103624.h1
Seq. No.	9004
Contig ID	15002_1.R1040
5'-most EST	uC-gmflminsoy091h05b1
Method	BLASTN
NCBI GI	g3746902
BLAST score	286
E value	1.0e-159
Match length	517
% identity	89
NCBI Description	Pisum sativum signal recognition particle 54 kDa subunit precursor (Ffc) mRNA, nuclear gene encoding chloroplast protein, partial cds
Seq. No.	9005
Contig ID	15004_1.R1040
5'-most EST	LIB3049-053-Q1-E1-A6
Seq. No.	9006
Contig ID	15007_1.R1040
5'-most EST	LIB3049-040-Q1-E1-G11
Method	BLASTX
NCBI GI	g1076387
BLAST score	789
E value	3.0e-84
Match length	181
% identity	83
NCBI Description	protein kinase homolog - Arabidopsis thaliana >gi_717180_emb_CAA55866_ (X79279) protein kinase homologous to shaggy and glycogen synthase kinase-3 [Arabidopsis thaliana]
Seq. No.	9007
Contig ID	15007_2.R1040
5'-most EST	fC-gmle700872092d2
Method	BLASTN
NCBI GI	g1504062
BLAST score	241
E value	1.0e-132
Match length	703
% identity	84
NCBI Description	A.thaliana mRNA for shaggy-like kinase kappa

Seq. No. 9008
 Contig ID 15007_3.R1040
 5'-most EST LIB3049-053-Q1-E1-A9
 Method BLASTX
 NCBI GI g1076387
 BLAST score 187
 E value 2.0e-18
 Match length 70
 % identity 73
 NCBI Description protein kinase homolog - Arabidopsis thaliana
 >gi_717180_emb_CAA55866_(X79279) protein kinase homologous
 to shaggy and glycogen synthase kinase-3 [Arabidopsis
 thaliana]

Seq. No. 9009
 Contig ID 15007_4.R1040
 5'-most EST LIB3109-012-Q1-K1-E6

Seq. No. 9010
 Contig ID 15008_1.R1040
 5'-most EST seb700652702.h1

Seq. No. 9011
 Contig ID 15008_2.R1040
 5'-most EST seb700652769.h1

Seq. No. 9012
 Contig ID 15008_3.R1040
 5'-most EST epX701106574.h1

Seq. No. 9013
 Contig ID 15013_1.R1040
 5'-most EST jC-gmst02400009b04a1

Seq. No. 9014
 Contig ID 15023_1.R1040
 5'-most EST uaw700664606.h1
 Method BLASTX
 NCBI GI g1255951
 BLAST score 1406
 E value 1.0e-156
 Match length 363
 % identity 75
 NCBI Description (X96932) PS60 [Nicotiana tabacum]

Seq. No. 9015
 Contig ID 15027_1.R1040
 5'-most EST LIB3138-071-P1-N1-B7
 Method BLASTX
 NCBI GI g3892056
 BLAST score 568
 E value 3.0e-58
 Match length 126
 % identity 87
 NCBI Description (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

09684016 IT 10000

Seq. No.	9034
Contig ID	15053_3.R1040
5'-most EST	LIB3050-008-Q1-E1-F5

Seq. No.	9036
Contig ID	15058_1.R1040
5'-most EST	LIB3073-004-Q1-K1-E12

Seq. No.	9038
Contig ID	15069_1.R1040
5'-most EST	LIB3049-052-Q1-E1-A7
Method	BLASTX
NCBI GI	g2244989
BLAST score	421
E value	3.0e-41
Match length	121
% identity	68
NCBI Description	(Z97340) strong similarity to naringenin 3-dioxygenase [Arabidopsis thaliana]

1617

Seq. No.	9059
Contig ID	15116_1.R1040
5'-most EST	LIB3049-051-Q1-E1-G11

Seq. No.	9060
Contig ID	15117_1.R1040
5'-most EST	LIB3170-032-Q1-K1-E12

```
Seq. No.          9061
Contig ID         15122_1.R1040
5'-most EST      epx701104947.h1
Method            BLASTX
NCBI GI           g3695023
BLAST score       149
E value           1.0e-09
Match length      46
% identity        57
NCBI Description  (AF055850) unknown [Arabidopsis thaliana]
```

```
Seq. No.          9062
Contig ID         15127_1.R1040
5'-most EST      LIB3072-051-Q1-E1-G1
```

Seq. No.	9063
Contig ID	15127_2.R1040
5'-most EST	LIB3072-043-Q1-K1-E10

```
Seq. No.          9064
Contig ID         15132_1.R1040
5'-most EST      pxt700945365.h1
Method            BLASTX
NCBI GI           g1706319
BLAST score       1231
E value           1.0e-135
Match length      393
% identity        58
NCBI Description  HISTIDINE DECARBOXYLASE (HDC) (TOM92)
                  >gi_481829_pir_S39554 histidine decarboxylase (EC
                  4.1.1.22) - tomato >gi_416534_emb_CAA50719_ (X71900)
                  histidine decarboxylase [Lycopersicon esculentum]
```

Seq. No.	9065
Contig ID	15132_2.R1040
5'-most EST	leu701149945.h1

Seq. No.	9066
Contig ID	15135_1.R1040
5'-most EST	q4396421

```
Seq. No.          9067
Contig ID         15141_1.R1040
5'-most EST      LIB3109-028-Q1-K1-H9
Method            BLASTN
NCBI GI           g3821780
BLAST score       33
E value           7.0e-09
```


Seq. No. 9102
 Contig ID 15237 1.R1040
 5'-most EST LIB3109-010-Q1-K1-C5

Seq. No. 9103
 Contig ID 15238 1.R1040
 5'-most EST LIB3170-034-Q1-K1-A8

Seq. No. 9104
 Contig ID 15239 1.R1040
 5'-most EST LIB3170-035-Q1-K1-B8

Seq. No. 9105
 Contig ID 15248 1.R1040
 5'-most EST LIB3049-050-Q1-E1-A12
 Method BLASTX
 NCBI GI g3063451
 BLAST score 451
 E value 9.0e-45
 Match length 194
 % identity 48
 NCBI Description (AC003981) F22O13.13 [Arabidopsis thaliana]

Seq. No. 9106
 Contig ID 15251 1.R1040
 5'-most EST LIB3049-050-Q1-E1-A6
 Method BLASTX
 NCBI GI g4406775
 BLAST score 363
 E value 1.0e-60
 Match length 358
 % identity 40
 NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 9107
 Contig ID 15253 1.R1040
 5'-most EST LIB3056-001-Q1-B1-G5
 Method BLASTX
 NCBI GI g3132470
 BLAST score 269
 E value 1.0e-23
 Match length 86
 % identity 57
 NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]

Seq. No. 9108
 Contig ID 15255 1.R1040
 5'-most EST leu701148356.h1
 Method BLASTX
 NCBI GI g3269297
 BLAST score 207
 E value 6.0e-16
 Match length 83
 % identity 47
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 9109

Match length	70
% identity	60
NCBI Description	germin type 2 - Arabidopsis thaliana >gi_1107491_emb_CAA63023_ (X91957) germin type2 [Arabidopsis thaliana]
Seq. No.	9115
Contig ID	15266_1.R1040
5'-most EST	jC-gmst02400053e08d1
Seq. No.	9116
Contig ID	15270_1.R1040
5'-most EST	LIB3072-057-Q1-K1-F6
Method	BLASTX
NCBI GI	g3786009
BLAST score	218
E value	2.0e-17
Match length	81
% identity	57
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.	9117
Contig ID	15272_1.R1040
5'-most EST	LIB3107-033-Q1-K1-C1
Method	BLASTN
NCBI GI	g2224730
BLAST score	256
E value	1.0e-141
Match length	556
% identity	89
NCBI Description	Vigna radiata mRNA for Aux22d, complete cds
Seq. No.	9118
Contig ID	15272_2.R1040
5'-most EST	kl1701212274.h1
Method	BLASTN
NCBI GI	g2224730
BLAST score	83
E value	6.0e-39
Match length	159
% identity	88
NCBI Description	Vigna radiata mRNA for Aux22d, complete cds
Seq. No.	9119
Contig ID	15274_1.R1040
5'-most EST	gsv701044983.h1
Method	BLASTX
NCBI GI	g1703574
BLAST score	470
E value	7.0e-47
Match length	185
% identity	47
NCBI Description	(U80437) C43E11.9 [Caenorhabditis elegans]
Seq. No.	9120
Contig ID	15281_1.R1040
5'-most EST	LIB3050-027-Q1-E1-H2

Method	BLASTX
NCBI GI	g2598597
BLAST score	249
E value	5.0e-21
Match length	101
% identity	50
NCBI Description	(Y15371) MtN5 [Medicago truncatula]

```
Seq. No.          9121
Contig ID         15281_2.R1040
5'-most EST      LIB3050-006-Q1-E1-F5
Method           BLASTX
NCBI GI          g2598597
BLAST score       315
E value          9.0e-29
Match length      101
% identity        58
NCBI Description  (Y15371) MtN5 [Medicago truncatula]
```

```
Seq. No.          9122
Contig ID         15281 3.R1040
5'-most EST      g5688280
Method            BLASTX
NCBI GI           g2598597
BLAST score       296
E value           1.0e-26
Match length      102
% identity        59
NCBI Description  (Y15371) MtN5 [Medicago truncatula]
```

```
Seq. No.          9123
Contig ID         15281 5.R1040
5'-most EST      LIB3107-022-Q1-K1-G6
Method           BLASTX
NCBI GI          g2598597
BLAST score      159
E value          8.0e-11
Match length     44
% identity       66
NCBI Description  (Y15371) MtN5 [Medicago truncatula]
```

Seq. No.	9124
Contig ID	15281_6.R1040
5'-most EST	uC-qmropic033q05b1

Seq. No.	9125
Contig ID	15284_1.R1040
5'-most EST	LIB3049-049-Q1-E1-F10

```
Seq. No.          9126
Contig ID         15285_1.R1040
5'-most EST      kll1701208201.h1
Method            BLASTN
NCBI GI           g1420935
BLAST score       243
E value           1.0e-134
Match length      472
```


09684016-1010000

% identity 88
NCBI Description Vigna unguiculata aspartic proteinase mRNA, complete cds
Seq. No. 9127
Contig ID 15291_1.R1040
5'-most EST LIB3170-035-Q1-K1-G7

Seq. No. 9128
Contig ID 15296_1.R1040
5'-most EST LIB3093-051-Q1-K1-E12
Method BLASTX
NCBI GI g2160183
BLAST score 431
E value 3.0e-42
Match length 134
% identity 67
NCBI Description (AC000132) Identical to A. thaliana U2 SnRNP-specific A' protein (gb_X69137). ESTs gb_ATTS0705, gb_ATTS0339 come from this gene. [Arabidopsis thaliana]

Seq. No. 9129
Contig ID 15300_1.R1040
5'-most EST taw700654794.h1
Method BLASTX
NCBI GI g2459442
BLAST score 360
E value 1.0e-33
Match length 223
% identity 43
NCBI Description (AC002332) putative DNA-binding protein PD1 [Arabidopsis thaliana]

Seq. No. 9130
Contig ID 15301_1.R1040
5'-most EST uC-gmronoir037e10b1
Method BLASTX
NCBI GI g2281633
BLAST score 473
E value 6.0e-47
Match length 184
% identity 57
NCBI Description (AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana]

Seq. No. 9131
Contig ID 15301_2.R1040
5'-most EST g5058437
Method BLASTX
NCBI GI g2281633
BLAST score 428
E value 2.0e-50
Match length 180
% identity 64
NCBI Description (AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana]

Seq. No. 9132

Contig ID	15301_3.R1040
5'-most EST	gsv701052436.h1
Seq. No.	9133
Contig ID	15317_1.R1040
5'-most EST	LIB3049-049-Q1-E1-A6
Seq. No.	9134
Contig ID	15318_1.R1040
5'-most EST	LIB3049-049-Q1-E1-A7
Method	BLASTX
NCBI GI	g1730109
BLAST score	382
E value	5.0e-37
Match length	99
% identity	81
NCBI Description	LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN HYDROXYLASE) >gi_499022_emb_CAA53580_(X75966) leucoanthocyanidin dioxygenase [Vitis vinifera]
Seq. No.	9135
Contig ID	15325_1.R1040
5'-most EST	LIB3170-036-Q1-K1-E7
Seq. No.	9136
Contig ID	15328_1.R1040
5'-most EST	LIB3093-036-Q1-K1-D8
Seq. No.	9137
Contig ID	15329_1.R1040
5'-most EST	LIB3092-014-Q1-K1-C10
Method	BLASTX
NCBI GI	g3434971
BLAST score	307
E value	2.0e-27
Match length	187
% identity	45
NCBI Description	(AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]
Seq. No.	9138
Contig ID	15329_2.R1040
5'-most EST	LIB3049-049-Q1-E1-B9
Method	BLASTX
NCBI GI	g3434971
BLAST score	237
E value	1.0e-19
Match length	67
% identity	69
NCBI Description	(AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]
Seq. No.	9139
Contig ID	15331_1.R1040
5'-most EST	ssr700559243.h1
Seq. No.	9140

NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No. 9148
Contig ID 15337_3.R1040
5'-most EST LIB3049-048-Q1-E1-H11

Seq. No. 9149
Contig ID 15339_1.R1040
5'-most EST jC-gmle01810046c08a1
Method BLASTX
NCBI GI g1730502
BLAST score 255
E value 9.0e-22
Match length 160
% identity 38
NCBI Description TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir_A31351 probable transmembrane protein FT27 - mouse >gi_535682 (M23568) transmembrane protein [Mus musculus]

Seq. No. 9150
Contig ID 15342_1.R1040
5'-most EST LIB3109-036-Q1-K1-F2
Method BLASTN
NCBI GI g3335331
BLAST score 41
E value 2.0e-13
Match length 189
% identity 80
NCBI Description Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 9151
Contig ID 15345_1.R1040
5'-most EST jC-gmro02800040f08a1
Method BLASTX
NCBI GI g1297187
BLAST score 373
E value 3.0e-35
Match length 170
% identity 46
NCBI Description (U53501) similar to protein encoded by GenBank Accession Number U41815, nucleoporin 98 [Arabidopsis thaliana]

Seq. No. 9152
Contig ID 15346_1.R1040
5'-most EST LIB3170-027-Q2-K1-G11
Method BLASTX
NCBI GI g3914667
BLAST score 451
E value 1.0e-44
Match length 136
% identity 72
NCBI Description 50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR >gi_2459427 (AC002332) putative chloroplast 50S ribosomal protein L28 [Arabidopsis thaliana]

Seq. No. 9153

Contig ID	15347_1.R1040
5'-most EST	jC-gmro02910035b06d1
Seq. No.	9154
Contig ID	15348_1.R1040
5'-most EST	LIB3170-033-Q1-K1-B7
Seq. No.	9155
Contig ID	15349_1.R1040
5'-most EST	LIB3072-061-Q1-K1-B1
Seq. No.	9156
Contig ID	15353_1.R1040
5'-most EST	LIB3049-048-Q1-E1-G9
Method	BLASTX
NCBI GI	g2708484
BLAST score	559
E value	1.0e-57
Match length	117
% identity	85
NCBI Description	(U79557) IAA24 [Arabidopsis thaliana]
Seq. No.	9157
Contig ID	15358_1.R1040
5'-most EST	LIB3049-048-Q1-E1-F7
Seq. No.	9158
Contig ID	15360_1.R1040
5'-most EST	LIB3170-034-Q1-K1-D6
Method	BLASTX
NCBI GI	g2827555
BLAST score	421
E value	2.0e-41
Match length	139
% identity	44
NCBI Description	(AL021635) Translation factor EF-1 alpha - like protein [Arabidopsis thaliana]
Seq. No.	9159
Contig ID	15361_1.R1040
5'-most EST	ncj700975258.h1
Method	BLASTX
NCBI GI	g3641837
BLAST score	809
E value	1.0e-86
Match length	243
% identity	70
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]
Seq. No.	9160
Contig ID	15363_1.R1040
5'-most EST	LIB3049-048-Q1-E1-G12
Seq. No.	9161
Contig ID	15364_1.R1040
5'-most EST	LIB3049-048-Q1-E1-G2

Seq. No. 9162
 Contig ID 15367_1.R1040
 5'-most EST uC-gmropic075g06b1
 Method BLASTX
 NCBI GI g3063457
 BLAST score 298
 E value 5.0e-27
 Match length 113
 % identity 55
 NCBI Description (AC003981) F22013.19 [Arabidopsis thaliana]

Seq. No. 9163
 Contig ID 15367_2.R1040
 5'-most EST jsh701064577.h1
 Method BLASTX
 NCBI GI g3063457
 BLAST score 165
 E value 2.0e-11
 Match length 99
 % identity 39
 NCBI Description (AC003981) F22013.19 [Arabidopsis thaliana]

Seq. No. 9164
 Contig ID 15368_1.R1040
 5'-most EST fua701041455.h1
 Method BLASTX
 NCBI GI g3551954
 BLAST score 607
 E value 9.0e-63
 Match length 245
 % identity 47
 NCBI Description (AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No. 9165
 Contig ID 15374_1.R1040
 5'-most EST LIB3049-048-Q1-E1-E1

Seq. No. 9166
 Contig ID 15375_1.R1040
 5'-most EST LIB3049-048-Q1-E1-E10

Seq. No. 9167
 Contig ID 15377_1.R1040
 5'-most EST LIB3053-011-Q1-N1-A4

Seq. No. 9168
 Contig ID 15380_1.R1040
 5'-most EST LIB3049-011-Q1-E1-B5
 Method BLASTX
 NCBI GI g3860274
 BLAST score 338
 E value 4.0e-31
 Match length 160
 % identity 42
 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Method	BLASTX
NCBI GI	g4220474
BLAST score	1493
E value	1.0e-166
Match length	487
% identity	66
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]
Seq. No.	9177
Contig ID	15402_2.R1040
5'-most EST	jC-gmro02800023b09d1
Seq. No.	9178
Contig ID	15404_1.R1040
5'-most EST	LIB3170-036-Q1-K2-C6
Seq. No.	9179
Contig ID	15408_1.R1040
5'-most EST	LIB3139-072-P1-N1-D6
Seq. No.	9180
Contig ID	15414_1.R1040
5'-most EST	LIB3170-036-Q1-K2-F6
Method	BLASTX
NCBI GI	g2315451
BLAST score	291
E value	7.0e-26
Match length	224
% identity	31
NCBI Description	(AF016448) No definition line found [Caenorhabditis elegans]
Seq. No.	9181
Contig ID	15417_1.R1040
5'-most EST	vwf700675916.h1
Method	BLASTN
NCBI GI	g12387
BLAST score	34
E value	2.0e-09
Match length	69
% identity	94
NCBI Description	Vicia faba chloroplast tRNA-Leu, tRNA-Phe, tRNA-His, ORFX, NADH-dehydrogenase genes & partial sequence ORFx & psbA genes
Seq. No.	9182
Contig ID	15420_1.R1040
5'-most EST	LIB3049-047-Q1-E1-G12
Seq. No.	9183
Contig ID	15425_1.R1040
5'-most EST	LIB3170-035-Q1-K1-H5
Seq. No.	9184
Contig ID	15426_1.R1040
5'-most EST	vwf700677929.h1

Method BLASTX
 NCBI GI g3236240
 BLAST score 947
 E value 1.0e-102
 Match length 428
 % identity 75
 NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 9185
 Contig ID 15426_2.R1040
 5'-most EST uC-gmropic041f01b1
 Method BLASTX
 NCBI GI g4099833
 BLAST score 227
 E value 3.0e-18
 Match length 70
 % identity 61
 NCBI Description (U90265) bifunctional nuclease [Zinnia elegans]

Seq. No. 9186
 Contig ID 15426_3.R1040
 5'-most EST leu701155823.h1
 Method BLASTX
 NCBI GI g3236240
 BLAST score 1071
 E value 1.0e-117
 Match length 292
 % identity 72
 NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 9187
 Contig ID 15426_4.R1040
 5'-most EST LIB3051-050-Q1-K1-B10
 Method BLASTX
 NCBI GI g3236240
 BLAST score 373
 E value 1.0e-35
 Match length 77
 % identity 91
 NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 9188
 Contig ID 15426_5.R1040
 5'-most EST zlv700807524.h1
 Method BLASTX
 NCBI GI g3236240
 BLAST score 604
 E value 1.0e-74
 Match length 175
 % identity 80
 NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 9189
 Contig ID 15426_9.R1040
 5'-most EST LIB3051-019-Q1-E1-C6
 Method BLASTX
 NCBI GI g3236240

09684015-101000

BLAST score 213
E value 2.0e-22
Match length 77
% identity 71
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 9190
Contig ID 15436_1.R1040
5'-most EST LIB3049-044-Q1-E1-E1

Seq. No. 9191
Contig ID 15436_2.R1040
5'-most EST LIB3109-022-Q1-K1-E12

Seq. No. 9192
Contig ID 15439_1.R1040
5'-most EST uC-gmflminsoy011d09b1

Seq. No. 9193
Contig ID 15441_1.R1040
5'-most EST LIB3073-006-Q1-K1-F10

Seq. No. 9194
Contig ID 15443_1.R1040
5'-most EST LIB3049-047-Q1-E1-F1

Seq. No. 9195
Contig ID 15445_1.R1040
5'-most EST LIB3051-003-Q1-E1-F12

Method BLASTX
NCBI GI g2129541
BLAST score 1586
E value 1.0e-177
Match length 474
% identity 67
NCBI Description ATPK19 protein - Arabidopsis thaliana >gi_914079_bbs_160872
ATPK19=ribosomal-protein S6 kinase homolog [Arabidopsis
thaliana, Peptide, 471 aa] >gi_867995_dbj_BAA07661
(D42061) ribosomal-protein S6 kinase homolog [Arabidopsis
thaliana]

Seq. No. 9196
Contig ID 15445_3.R1040
5'-most EST jC-gmle01810020b07d1

Method BLASTX
NCBI GI g2129541
BLAST score 219
E value 9.0e-18
Match length 63
% identity 65
NCBI Description ATPK19 protein - Arabidopsis thaliana >gi_914079_bbs_160872
ATPK19=ribosomal-protein S6 kinase homolog [Arabidopsis
thaliana, Peptide, 471 aa] >gi_867995_dbj_BAA07661
(D42061) ribosomal-protein S6 kinase homolog [Arabidopsis
thaliana]

Seq. No. 9197

09684036-101000

5'-most EST LIB3170-033-Q1-K1-F5

Seq. No. 9204
 Contig ID 15456_1.R1040
 5'-most EST LIB3087-002-Q1-K1-A7
 Method BLASTX
 NCBI GI g3600051
 BLAST score 185
 E value 2.0e-13
 Match length 44
 % identity 77
 NCBI Description (AF080120) contains similarity to the single-strand binding proteins family (Pfam: SSB.hmm, score: 24.02) [Arabidopsis thaliana]

Seq. No. 9205
 Contig ID 15463_1.R1040
 5'-most EST LIB3049-047-Q1-E1-D11
 Method BLASTX
 NCBI GI g4138581
 BLAST score 275
 E value 2.0e-24
 Match length 131
 % identity 21
 NCBI Description (X98474) mitochondrial energy transfer protein [Solanum tuberosum]

Seq. No. 9206
 Contig ID 15466_1.R1040
 5'-most EST LIB3092-011-Q1-K1-C5
 Method BLASTN
 NCBI GI g3985934
 BLAST score 53
 E value 8.0e-21
 Match length 279
 % identity 83
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No. 9207
 Contig ID 15467_1.R1040
 5'-most EST LIB3049-047-Q1-E1-D5

Seq. No. 9208
 Contig ID 15476_1.R1040
 5'-most EST LIB3170-033-Q1-K1-E5
 Method BLASTX
 NCBI GI g1168251
 BLAST score 416
 E value 9.0e-41
 Match length 95
 % identity 79
 NCBI Description PROBABLE CYSTEINE PROTEINASE A494 PRECURSOR
 >gi_1076384_pir_S46535 probable cysteine proteinase (EC 3.4.22.-) (clone A1494) - Arabidopsis thaliana (fragment)
 >gi_516865_emb_CAA52403_ (X74359) putative thiol protease [Arabidopsis thaliana]

E value 8.0e-64
 Match length 163
 % identity 72
 NCBI Description (AL049487) hypothetical protein [Arabidopsis thaliana]

Seq. No. 9219
 Contig ID 15499_1.R1040
 5'-most EST hyd700725239.h1
 Method BLASTX
 NCBI GI g2911047
 BLAST score 400
 E value 8.0e-39
 Match length 112
 % identity 73
 NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 9220
 Contig ID 15500_1.R1040
 5'-most EST LIB3109-022-Q1-K1-C2

Seq. No. 9221
 Contig ID 15500_2.R1040
 5'-most EST LIB3051-104-Q1-K1-C6

Seq. No. 9222
 Contig ID 15500_3.R1040
 5'-most EST fC-gmf1700907636a1

Seq. No. 9223
 Contig ID 15507_1.R1040
 5'-most EST LIB3049-046-Q1-E1-F5
 Method BLASTX
 NCBI GI g4335725
 BLAST score 236
 E value 8.0e-20
 Match length 85
 % identity 56
 NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. 9224
 Contig ID 15513_1.R1040
 5'-most EST LIB3138-090-P1-N1-A6
 Method BLASTX
 NCBI GI g2827699
 BLAST score 447
 E value 6.0e-44
 Match length 278
 % identity 44
 NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 9225
 Contig ID 15515_1.R1040
 5'-most EST LIB3170-033-Q1-K1-A5

Seq. No. 9226
 Contig ID 15516_1.R1040
 5'-most EST LIB3049-046-Q1-E1-G4

09684016 101000

Seq. No. 9227
Contig ID 15518_1.R1040
5'-most EST LIB3049-046-Q1-E1-G7
Method BLASTN
NCBI GI g3421089
BLAST score 270
E value 1.0e-150
Match length 654
% identity 85
NCBI Description Arabidopsis thaliana 20S proteasome subunit PAE2 (PAE2)
mRNA, complete cds

Seq. No. 9228
Contig ID 15518_2.R1040
5'-most EST LIB3170-052-Q1-J1-F7

Seq. No. 9229
Contig ID 15518_3.R1040
5'-most EST LIB3051-029-Q1-K1-B3
Method BLASTN
NCBI GI g3421089
BLAST score 125
E value 8.0e-64
Match length 333
% identity 85
NCBI Description Arabidopsis thaliana 20S proteasome subunit PAE2 (PAE2)
mRNA, complete cds

Seq. No. 9230
Contig ID 15518_4.R1040
5'-most EST fua701039082.h1
Method BLASTX
NCBI GI g3421090
BLAST score 224
E value 3.0e-36
Match length 101
% identity 79
NCBI Description (AF043525) 20S proteasome subunit PAE2 [Arabidopsis
thaliana]

Seq. No. 9231
Contig ID 15523_1.R1040
5'-most EST uC-gmflminsoy018c06b1
Method BLASTX
NCBI GI g2129559
BLAST score 754
E value 3.0e-80
Match length 181
% identity 80
NCBI Description cellulase homolog OR16pep - Arabidopsis thaliana
>gi_1022807 (U37702) cellulase [Arabidopsis thaliana]
>gi_3493633 (AF074092) cellulase [Arabidopsis thaliana]
>gi_3598956 (AF074375) cellulase [Arabidopsis thaliana]
>gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
[Arabidopsis thaliana]

NCBI GI g1946367
 BLAST score 215
 E value 6.0e-17
 Match length 65
 % identity 62
 NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 9239
 Contig ID 15535_2.R1040
 5'-most EST uC-gmflminsoy040a03b1
 Method BLASTX
 NCBI GI g1946367
 BLAST score 611
 E value 2.0e-63
 Match length 164
 % identity 70
 NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 9240
 Contig ID 15537_1.R1040
 5'-most EST jC-gmro02910061h09a1
 Method BLASTX
 NCBI GI g3724328
 BLAST score 144
 E value 1.0e-08
 Match length 160
 % identity 27
 NCBI Description (AB013095) heme-binding protein [Mus musculus]

Seq. No. 9241
 Contig ID 15541_1.R1040
 5'-most EST LIB3049-046-Q1-E1-C3

Seq. No. 9242
 Contig ID 15541_2.R1040
 5'-most EST LIB3072-061-Q1-K1-A2

Seq. No. 9243
 Contig ID 15542_1.R1040
 5'-most EST pcp700993990.h1

Seq. No. 9244
 Contig ID 15546_1.R1040
 5'-most EST LIB3170-028-Q1-K1-B12

Seq. No. 9245
 Contig ID 15546_2.R1040
 5'-most EST leu701147556.h1

Seq. No. 9246
 Contig ID 15550_1.R1040
 5'-most EST LIB3170-034-Q1-K1-B4

Seq. No. 9247
 Contig ID 15550_2.R1040
 5'-most EST LIB3138-097-Q1-N1-F10

Seq. No. 9248
 Contig ID 15551_1.R1040
 5'-most EST LIB3049-046-Q1-E1-B9
 Method BLASTX
 NCBI GI g1706311
 BLAST score 376
 E value 5.0e-36
 Match length 189
 % identity 43
 NCBI Description PROBABLE ATP-DEPENDENT RNA HELICASE DBP1 (HELICASE CA1)
 >gi_2132404_pir_S62003 probable ATP-dependent RNA helicase
 DBP1 - yeast (*Saccharomyces cerevisiae*) >gi_1163095
 (U43503) Dbp1p, Lph8p [*Saccharomyces cerevisiae*]

Seq. No. 9249
 Contig ID 15557_1.R1040
 5'-most EST zsg701119272.h1

Seq. No. 9250
 Contig ID 15560_1.R1040
 5'-most EST LIB3170-033-Q1-K1-D4
 Method BLASTX
 NCBI GI g1076715
 BLAST score 239
 E value 9.0e-20
 Match length 82
 % identity 50
 NCBI Description abscisic acid-induced protein HVA22 - barley >gi_404589
 (L19119) A22 [*Hordeum vulgare*]

Seq. No. 9251
 Contig ID 15561_1.R1040
 5'-most EST fua701043583.h1
 Method BLASTX
 NCBI GI g2252631
 BLAST score 263
 E value 7.0e-23
 Match length 83
 % identity 63
 NCBI Description (U95973) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 9252
 Contig ID 15561_2.R1040
 5'-most EST trc700561886.h1

Seq. No. 9253
 Contig ID 15565_1.R1040
 5'-most EST LIB3049-046-Q1-E1-B3
 Method BLASTX
 NCBI GI g2288985
 BLAST score 216
 E value 3.0e-17
 Match length 94
 % identity 18
 NCBI Description (AC002335) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 9254

Seq. No.	9263
Contig ID	15598_1.R1040
5'-most EST	uC-gmrominsoy060e11b1
Method	BLASTX
NCBI GI	g4469026
BLAST score	294
E value	2.0e-26
Match length	106
% identity	60
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.	9264
Contig ID	15598_2.R1040
5'-most EST	pcp700991182.h1
Method	BLASTX
NCBI GI	g4469026
BLAST score	185
E value	9.0e-14
Match length	70
% identity	60
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.	9265
Contig ID	15605_1.R1040
5'-most EST	smc700747914.h1
Seq. No.	9266
Contig ID	15605_2.R1040
5'-most EST	k11701206351.h1
Seq. No.	9267
Contig ID	15610_1.R1040
5'-most EST	LIB3170-034-Q1-K1-F8
Seq. No.	9268
Contig ID	15612_1.R1040
5'-most EST	crh700852730.h1
Method	BLASTX
NCBI GI	g4263707
BLAST score	819
E value	1.0e-110
Match length	307
% identity	64
NCBI Description	(AC006223) putative 70kD heat shock protein [Arabidopsis thaliana]
Seq. No.	9269
Contig ID	15613_1.R1040
5'-most EST	uC-gmronoir0001c11a1
Method	BLASTX
NCBI GI	g4337044
BLAST score	319
E value	2.0e-29
Match length	90
% identity	69
NCBI Description	(AF124161) molybdopterin synthase sulphurylase [Nicotiana plumbaginifolia]

Seq. No. 9270
 Contig ID 15613_2.R1040
 5'-most EST LIB3049-045-Q1-E1-E4
 Method BLASTX
 NCBI GI g4337044
 BLAST score 297
 E value 5.0e-27
 Match length 86
 % identity 65
 NCBI Description (AF124161) molybdopterin synthase sulphurylase [Nicotiana plumbaginifolia]

Seq. No. 9271
 Contig ID 15614_1.R1040
 5'-most EST LIB3170-036-Q1-J1-F11

Seq. No. 9272
 Contig ID 15615_1.R1040
 5'-most EST LIB3109-014-Q1-K1-A8
 Method BLASTX
 NCBI GI g2982243
 BLAST score 475
 E value 3.0e-47
 Match length 158
 % identity 58
 NCBI Description (AF051204) hypothetical protein [Picea mariana]

Seq. No. 9273
 Contig ID 15615_2.R1040
 5'-most EST LIB3107-029-Q1-K1-E11
 Method BLASTX
 NCBI GI g2982243
 BLAST score 187
 E value 7.0e-14
 Match length 69
 % identity 54
 NCBI Description (AF051204) hypothetical protein [Picea mariana]

Seq. No. 9274
 Contig ID 15615_4.R1040
 5'-most EST LIB3109-055-Q1-K1-F5
 Method BLASTX
 NCBI GI g2982243
 BLAST score 196
 E value 4.0e-15
 Match length 93
 % identity 45
 NCBI Description (AF051204) hypothetical protein [Picea mariana]

Seq. No. 9275
 Contig ID 15617_1.R1040
 5'-most EST LIB3094-011-Q1-K1-E3
 Method BLASTN
 NCBI GI g21045
 BLAST score 214
 E value 1.0e-116

Match length 691
 % identity 61
 NCBI Description P.vulgaris mRNA for prolin-rich protein (PvPRP1)

Seq. No. 9276
 Contig ID 15617_2.R1040
 5'-most EST asn701135096.h1
 Method BLASTN
 NCBI GI g21045
 BLAST score 35
 E value 3.0e-10
 Match length 93
 % identity 90
 NCBI Description P.vulgaris mRNA for prolin-rich protein (PvPRP1)

Seq. No. 9277
 Contig ID 15620_1.R1040
 5'-most EST rca700998350.h1
 Method BLASTX
 NCBI GI g4191782
 BLAST score 548
 E value 2.0e-56
 Match length 124
 % identity 86
 NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No. 9278
 Contig ID 15621_1.R1040
 5'-most EST LIB3072-053-Q1-E1-D8

Seq. No. 9279
 Contig ID 15623_1.R1040
 5'-most EST wrg700791003.h1
 Method BLASTX
 NCBI GI g3461884
 BLAST score 340
 E value 1.0e-31
 Match length 95
 % identity 72
 NCBI Description (AB006082) phosphoribosyl-ATP pyrophosphohydrolase
 [Arabidopsis thaliana] >gi_3461886_dbj_BAA32529_ (AB006083)
 phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis
 thaliana]

Seq. No. 9280
 Contig ID 15626_1.R1040
 5'-most EST LIB3170-087-Q1-K1-C5
 Method BLASTX
 NCBI GI g2706450
 BLAST score 903
 E value 2.0e-97
 Match length 216
 % identity 81
 NCBI Description (AJ225172) magnesium dependent soluble inorganic
 pyrophosphatase [Solanum tuberosum]

Seq. No. 9281

0001016 " 101000

NCBI Description (AF096370) similar to inorganic pyrophosphatase (Pfam: PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis thaliana]

Seq. No. 9286
Contig ID 15627_1.R1040
5'-most EST jC-gmro02800032f02a1
Method BLASTX
NCBI GI g3775999
BLAST score 472
E value 6.0e-47
Match length 102
% identity 86

NCBI Description (AJ010463) RNA helicase [Arabidopsis thaliana]

Seq. No. 9287
Contig ID 15632_1.R1040
5'-most EST jC-gmle01810091a04d1
Method BLASTX
NCBI GI g3702321
BLAST score 541
E value 3.0e-55
Match length 114
% identity 88

NCBI Description (AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]

Seq. No. 9288
Contig ID 15632_2.R1040
5'-most EST jC-gmro02910046d09d1
Method BLASTX
NCBI GI g3702321
BLAST score 453
E value 3.0e-45
Match length 91
% identity 93

NCBI Description (AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]

Seq. No. 9289
Contig ID 15635_1.R1040
5'-most EST leu70l145544.h1
Method BLASTX
NCBI GI g3063698
BLAST score 551
E value 2.0e-56
Match length 179
% identity 61

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 9290
Contig ID 15642_1.R1040
5'-most EST LIB3049-045-Q1-E1-A3

Seq. No. 9291
Contig ID 15645_1.R1040
5'-most EST LIB3138-073-P1-N1-C9

000T0T"9T048960

NCBI Description Pisum sativum mitochondrial rpl5, rps14 and cob genes

Seq. No. 9313
 Contig ID 15692_1.R1040
 5'-most EST kl1701202946.h1
 Method BLASTX
 NCBI GI g3063695
 BLAST score 321
 E value 2.0e-29
 Match length 109
 % identity 62
 NCBI Description (AL022537) hypothetical protein [Arabidopsis thaliana]

Seq. No. 9314
 Contig ID 15701_1.R1040
 5'-most EST LIB3049-044-Q1-E1-E12
 Method BLASTX
 NCBI GI g2346988
 BLAST score 174
 E value 3.0e-12
 Match length 98
 % identity 25
 NCBI Description (AB006606) ZPT4-4 [Petunia x hybrida]

Seq. No. 9315
 Contig ID 15704_1.R1040
 5'-most EST uC-gmrominsoy318b03b1
 Method BLASTN
 NCBI GI g11303
 BLAST score 637
 E value 0.0e+00
 Match length 725
 % identity 97
 NCBI Description G.max chloroplast mRNA for ndhK polypeptide and orf 158/159

Seq. No. 9316
 Contig ID 15704_2.R1040
 5'-most EST LIB3109-031-Q1-K1-E4
 Method BLASTN
 NCBI GI g881440
 BLAST score 232
 E value 1.0e-127
 Match length 328
 % identity 93
 NCBI Description Lupinus luteus NADH-plastoquinone oxidoreductase (ndhC) gene, chloroplast gene encoding chloroplast protein, complete cds

Seq. No. 9317
 Contig ID 15706_1.R1040
 5'-most EST hrw701058184.h1
 Method BLASTX
 NCBI GI g3320120
 BLAST score 162
 E value 6.0e-11
 Match length 65
 % identity 48

5'-most EST dkc700968011.h1
 Method BLASTX
 NCBI GI g2245138
 BLAST score 858
 E value 4.0e-92
 Match length 258
 % identity 70
 NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 9332
 Contig ID 15742_2.R1040
 5'-most EST jC-gmst02400025c09a1
 Method BLASTX
 NCBI GI g2245138
 BLAST score 374
 E value 8.0e-36
 Match length 121
 % identity 64
 NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 9333
 Contig ID 15749_1.R1040
 5'-most EST LIB3049-043-Q1-E1-H1

Seq. No. 9334
 Contig ID 15754_1.R1040
 5'-most EST wvk700682131.h1
 Method BLASTX
 NCBI GI g3668080
 BLAST score 912
 E value 2.0e-98
 Match length 289
 % identity 67
 NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 9335
 Contig ID 15754_2.R1040
 5'-most EST LIB3106-063-Q1-K1-C9

Seq. No. 9336
 Contig ID 15757_1.R1040
 5'-most EST LIB3170-035-Q1-K1-D2

Seq. No. 9337
 Contig ID 15759_1.R1040
 5'-most EST LIB3093-044-Q1-K1-F3
 Method BLASTX
 NCBI GI g4091117
 BLAST score 535
 E value 2.0e-54
 Match length 171
 % identity 62
 NCBI Description (AF047428) nucleic acid binding protein [Oryza sativa]

Seq. No. 9338
 Contig ID 15759_2.R1040
 5'-most EST LIB3049-043-Q1-E1-G2

09634316 1000

Seq. No.	9361
Contig ID	15840_1.R1040
5'-most EST	LIB3049-042-Q1-E1-G4
Method	BLASTX
NCBI GI	g3738289
BLAST score	416
E value	1.0e-40
Match length	116
% identity	69
NCBI Description	(AC005309) Not56-like protein [Arabidopsis thaliana]

```
Seq. No.          9363
Contig ID         15857_1.R1040
5'-most EST      LIB3049-042-Q1-E1-F10
Method           BLASTX
NCBI GI          g3894191
BLAST score       194
E value          8.0e-15
Match length      102
% identity        41
NCBI Description  (AC005662) unknown protein [Arabidopsis thaliana]
```

Seq. No.	9365
Contig ID	15872_1.R1040
5'-most EST	LIB3139-004-P1-N1-D1

Seq. No.	9367
Contig ID	15875_1.R1040
5'-most EST	uC-gmf̄lminsoy031a04b1

Method	BLASTX
NCBI GI	g2505874
BLAST score	1051
E value	1.0e-119
Match length	250
% identity	80
NCBI Description	(Y12776) putative kinase [Arabidopsis thaliana]
Seq. No.	9373
Contig ID	15894_1.R1040
5'-most EST	LIB3073-014-Q1-K1-E8
Seq. No.	9374
Contig ID	15894_2.R1040
5'-most EST	jsh701067288.h1
Seq. No.	9375
Contig ID	15894_3.R1040
5'-most EST	LIB3073-013-Q1-K1-E8
Seq. No.	9376
Contig ID	15894_4.R1040
5'-most EST	jC-gmst02400008a10a1
Seq. No.	9377
Contig ID	15894_5.R1040
5'-most EST	seb700651282.h1
Seq. No.	9378
Contig ID	15898_1.R1040
5'-most EST	pxt700944642.h1
Method	BLASTX
NCBI GI	g3540197
BLAST score	211
E value	1.0e-16
Match length	72
% identity	56
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]
Seq. No.	9379
Contig ID	15900_1.R1040
5'-most EST	LIB3170-024-Q1-K1-E1
Method	BLASTX
NCBI GI	g4336747
BLAST score	416
E value	2.0e-40
Match length	281
% identity	36
NCBI Description	(AF104924) unconventional myosin heavy chain [Zea mays]
Seq. No.	9380
Contig ID	15901_1.R1040
5'-most EST	LIB3049-041-Q1-E1-H5
Method	BLASTX
NCBI GI	g2245128
BLAST score	438
E value	3.0e-43

Match length 126
 % identity 65
 NCBI Description (Z97344) peroxidase [Arabidopsis thaliana]

Seq. No. 9381
 Contig ID 15902_1.R1040
 5'-most EST hyd700727214.h1

Seq. No. 9382
 Contig ID 15902_2.R1040
 5'-most EST zsg701120876.h1

Method BLASTX
 NCBI GI g2351846
 BLAST score 269
 E value 2.0e-23

Match length 111
 % identity 52

NCBI Description (U93050) poly(A) binding protein II [Mus musculus]

Seq. No. 9383
 Contig ID 15910_1.R1040
 5'-most EST uC-gmropic044c11b1

Method BLASTX
 NCBI GI g4415942
 BLAST score 240
 E value 2.0e-35

Match length 161
 % identity 53

NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No. 9384
 Contig ID 15910_2.R1040
 5'-most EST LIB3139-050-P1-N1-B6

Method BLASTX
 NCBI GI g4415942
 BLAST score 226
 E value 3.0e-18

Match length 118
 % identity 39

NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No. 9385
 Contig ID 15913_1.R1040
 5'-most EST k11701211472.h1

Method BLASTX
 NCBI GI g4432855
 BLAST score 1127
 E value 1.0e-123

Match length 339
 % identity 71

NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 9386
 Contig ID 15915_1.R1040
 5'-most EST LIB3170-041-Q1-K1-B3

Method BLASTN
 NCBI GI g3046856

BLAST score 57
 E value 4.0e-23
 Match length 141
 % identity 86
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 MXI22, complete sequence [Arabidopsis thaliana]

Seq. No. 9387
 Contig ID 15917_1.R1040
 5'-most EST LIB3049-040-Q1-E1-H6
 Method BLASTX
 NCBI GI g1362078
 BLAST score 578
 E value 2.0e-59
 Match length 216
 % identity 60
 NCBI Description endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
 - common nasturtium >gi_311835_emb_CAA48324_ (X68254)
 cellulase [Tropaeolum majus]

Seq. No. 9388
 Contig ID 15921_1.R1040
 5'-most EST LIB3138-023-Q1-N1-G4
 Method BLASTX
 NCBI GI g2920839
 BLAST score 337
 E value 2.0e-31
 Match length 129
 % identity 51
 NCBI Description (U95136) Os-FIERG2 gene product [Oryza sativa]

Seq. No. 9389
 Contig ID 15924_1.R1040
 5'-most EST LIB3093-024-Q1-K1-A6
 Method BLASTX
 NCBI GI g3063709
 BLAST score 358
 E value 5.0e-34
 Match length 135
 % identity 61
 NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 9390
 Contig ID 15926_1.R1040
 5'-most EST LIB3170-022-Q1-K1-E6
 Method BLASTN
 NCBI GI g3985958
 BLAST score 41
 E value 2.0e-13
 Match length 290
 % identity 82
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 MZN1, complete sequence [Arabidopsis thaliana]

Seq. No. 9391
 Contig ID 15926_3.R1040
 5'-most EST LIB3170-032-Q1-K1-E4

Method BLASTN
 NCBI GI g3985958
 BLAST score 33
 E value 5.0e-09
 Match length 182
 % identity 82
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MN1, complete sequence [Arabidopsis thaliana]

Seq. No. 9392
 Contig ID 15931_1.R1040
 5'-most EST LIB3049-041-Q1-E1-G9
 Method BLASTX
 NCBI GI g3914156
 BLAST score 357
 E value 6.0e-34
 Match length 94
 % identity 70
 NCBI Description NUCLEOLAR PROTEIN AT BAND 60B >gi_2661227 (AF017230) nucleolar protein at band 60B [Drosophila melanogaster] >gi_4322557_gb AAD16092_ (AF089837) minifly protein [Drosophila melanogaster]

Seq. No. 9393
 Contig ID 15939_1.R1040
 5'-most EST LIB3073-013-Q1-K1-C10
 Method BLASTX
 NCBI GI g4559358
 BLAST score 422
 E value 2.0e-41
 Match length 100
 % identity 77
 NCBI Description (AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No. 9394
 Contig ID 15939_2.R1040
 5'-most EST LIB3049-041-Q1-E1-E11
 Method BLASTX
 NCBI GI g4559358
 BLAST score 398
 E value 1.0e-38
 Match length 99
 % identity 73
 NCBI Description (AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No. 9395
 Contig ID 15941_1.R1040
 5'-most EST gbt700547911.h1

Seq. No. 9396
 Contig ID 15942_1.R1040
 5'-most EST LIB3049-041-Q1-E1-E3

Seq. No. 9397
 Contig ID 15950_1.R1040

09684016-1010000

5'-most EST taw700656026.h1
 Method BLASTX
 NCBI GI g2244822
 BLAST score 235
 E value 2.0e-19
 Match length 63
 % identity 70
 NCBI Description (Z97336) RNA polymerase II fifth largest subunit homolog
 [Arabidopsis thaliana]

Seq. No. 9398
 Contig ID 15952_1.R1040
 5'-most EST LIB3049-016-Q1-E1-C3
 Method BLASTX
 NCBI GI g2896687
 BLAST score 165
 E value 2.0e-11
 Match length 87
 % identity 48
 NCBI Description (AL021897) hypothetical protein Rv1050 [Mycobacterium
 tuberculosis]

Seq. No. 9399
 Contig ID 15952_2.R1040
 5'-most EST fde700876935.h1

Seq. No. 9400
 Contig ID 15953_1.R1040
 5'-most EST jC-gmro02910005e12d1
 Method BLASTX
 NCBI GI g3033400
 BLAST score 245
 E value 4.0e-20
 Match length 104
 % identity 50
 NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis
 thaliana]

Seq. No. 9401
 Contig ID 15955_1.R1040
 5'-most EST fua701038882.h1
 Method BLASTX
 NCBI GI g2827699
 BLAST score 422
 E value 3.0e-41
 Match length 206
 % identity 52
 NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 9402
 Contig ID 15955_2.R1040
 5'-most EST crh700853141.h1
 Method BLASTX
 NCBI GI g2827699
 BLAST score 120
 E value 7.0e-14
 Match length 106

Seq. No. 9413
 Contig ID 15995_1.R1040
 5'-most EST nsy700645633.h1
 Method BLASTN
 NCBI GI g3868852
 BLAST score 268
 E value 1.0e-149
 Match length 588
 % identity 88
 NCBI Description *Vigna radiata* ARG8 mRNA for GPI-anchored protein, complete cds

Seq. No. 9414
 Contig ID 15995_2.R1040
 5'-most EST ssr700557224.h1

Seq. No. 9415
 Contig ID 15995_3.R1040
 5'-most EST LIB3049-040-Q1-E1-G2
 Method BLASTN
 NCBI GI g3868852
 BLAST score 103
 E value 1.0e-50
 Match length 333
 % identity 84
 NCBI Description *Vigna radiata* ARG8 mRNA for GPI-anchored protein, complete cds

Seq. No. 9416
 Contig ID 15995_4.R1040
 5'-most EST LIB3093-018-Q1-K1-H7
 Method BLASTN
 NCBI GI g3868852
 BLAST score 155
 E value 1.0e-81
 Match length 293
 % identity 89
 NCBI Description *Vigna radiata* ARG8 mRNA for GPI-anchored protein, complete cds

Seq. No. 9417
 Contig ID 15996_1.R1040
 5'-most EST ncj700988212.h1
 Method BLASTX
 NCBI GI g2655037
 BLAST score 274
 E value 4.0e-36
 Match length 261
 % identity 35
 NCBI Description (AF019952) tumor suppressing STF cDNA 1 [*Homo sapiens*]
 >gi_4507703_ref_NP_003301.1_pTSSC1_tumor suppressing
 subtransferable candidate

Seq. No. 9418
 Contig ID 15997_1.R1040
 5'-most EST uxk700671968.h1

5'-most EST	LIB3049-039-Q1-E1-G1
Method	BLASTX
NCBI GI	g3860255
BLAST score	222
E value	6.0e-18
Match length	128
% identity	41
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]
Seq. No.	9451
Contig ID	16083_1.R1040
5'-most EST	gsv701054107.h1
Method	BLASTN
NCBI GI	g3869074
BLAST score	38
E value	1.0e-11
Match length	50
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MM19, complete sequence [Arabidopsis thaliana]
Seq. No.	9452
Contig ID	16089_1.R1040
5'-most EST	LIB3049-039-Q1-E1-G7
Seq. No.	9453
Contig ID	16090_1.R1040
5'-most EST	LIB3049-039-Q1-E1-G9
Seq. No.	9454
Contig ID	16093_1.R1040
5'-most EST	LIB3139-026-P1-N1-H3
Method	BLASTX
NCBI GI	g1532163
BLAST score	211
E value	2.0e-16
Match length	90
% identity	50
NCBI Description	(U63815) similar to glutaredoxin encoded by GenBank Accession Number Z49699; localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initiation codon and stop c
Seq. No.	9455
Contig ID	16093_2.R1040
5'-most EST	LIB3049-039-Q1-E1-E1
Seq. No.	9456
Contig ID	16095_1.R1040
5'-most EST	LIB3170-029-Q1-K1-G10
Seq. No.	9457
Contig ID	16101_1.R1040
5'-most EST	sat701008810.h1
Method	BLASTX
NCBI GI	g2191150

Seq. No. 9478
 Contig ID 16144_2.R1040
 5'-most EST LIB3072-054-Q1-E1-E9

Seq. No. 9479
 Contig ID 16145_1.R1040
 5'-most EST uC-gmrominsoy157e03b1
 Method BLASTX
 NCBI GI g2665890
 BLAST score 2241
 E value 0.0e+00
 Match length 534
 % identity 81
 NCBI Description (AF035944) calcium-dependent protein kinase [Fragaria x ananassa]

Seq. No. 9480
 Contig ID 16147_1.R1040
 5'-most EST LIB3049-034-Q1-E1-F8
 Method BLASTX
 NCBI GI g729538
 BLAST score 243
 E value 3.0e-20
 Match length 103
 % identity 54
 NCBI Description FERREDOXIN-THIOREDOXIN REDUCTASE, VARIABLE CHAIN PRECURSOR (FTR-V) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT A) (FTR-A) >gi_2144358_pir_RDSPTA ferredoxin--thioredoxin reductase (EC 1.18.-.-) chain A precursor - spinach >gi_474766_emb_CAA55480_ (X78880) ferredoxin:thioredoxin reductase [Spinacia oleracea] >gi_861138_emb_CAA54408_ (X77163) ferredoxin-thioredoxin reductase SU A [Spinacia oleracea]

Seq. No. 9481
 Contig ID 16147_2.R1040
 5'-most EST smc700745464.h1
 Method BLASTX
 NCBI GI g1362192
 BLAST score 195
 E value 1.0e-14
 Match length 64
 % identity 53
 NCBI Description ferredoxin--thioredoxin reductase (EC 1.18.-.-) variable chain - maize

Seq. No. 9482
 Contig ID 16148_1.R1040
 5'-most EST LIB3170-032-Q1-K1-B5

Seq. No. 9483
 Contig ID 16148_2.R1040
 5'-most EST vwf700675339.h1

Seq. No. 9484
 Contig ID 16148_3.R1040
 5'-most EST txt700733039.h1

Contig ID 16170_1.R1040
 5'-most EST LIB3170-030-Q1-K1-H9
 Method BLASTX
 NCBI GI g2583123
 BLAST score 450
 E value 6.0e-45
 Match length 122
 % identity 75
 NCBI Description (AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No. 9492
 Contig ID 16171_1.R1040
 5'-most EST LIB3170-032-Q1-K1-A5
 Method BLASTX
 NCBI GI g730692
 BLAST score 234
 E value 2.0e-19
 Match length 122
 % identity 44
 NCBI Description RUBISCO-ASSOCIATED PROTEIN >gi_454179 (L28804) putative [Glycine max] >gi_1090839_prf__2019481A RuBisCO complex protein [Glycine max]

Seq. No. 9493
 Contig ID 16173_1.R1040
 5'-most EST LIB3109-028-Q1-K1-D6
 Method BLASTX
 NCBI GI g4325282
 BLAST score 362
 E value 2.0e-47
 Match length 109
 % identity 86
 NCBI Description (AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No. 9494
 Contig ID 16176_1.R1040
 5'-most EST LIB3170-030-Q1-K1-A9

Seq. No. 9495
 Contig ID 16177_1.R1040
 5'-most EST jC-gmst02400065b11a2

Seq. No. 9496
 Contig ID 16177_2.R1040
 5'-most EST zhf700952970.h1

Seq. No. 9497
 Contig ID 16180_1.R1040
 5'-most EST LIB3049-038-Q1-E1-E8

Seq. No. 9498
 Contig ID 16183_1.R1040
 5'-most EST LIB3106-092-Q1-K1-F6

Seq. No. 9499
 Contig ID 16186_1.R1040
 5'-most EST ssr700553976.h1
 Method BLASTX
 NCBI GI g1171577
 BLAST score 337
 E value 2.0e-31
 Match length 166
 % identity 42
 NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 9500
 Contig ID 16188_1.R1040
 5'-most EST LIB3170-031-Q1-J1-D9

Seq. No. 9501
 Contig ID 16198_1.R1040
 5'-most EST LIB3049-038-Q1-E1-D1
 Method BLASTN
 NCBI GI g558628
 BLAST score 441
 E value 0.0e+00
 Match length 978
 % identity 90
 NCBI Description P.vulgaris mRNA for RNP1 chloroplast RNA binding protein

Seq. No. 9502
 Contig ID 16198_2.R1040
 5'-most EST LIB3106-108-Q1-K1-A2
 Method BLASTN
 NCBI GI g558628
 BLAST score 71
 E value 1.0e-31
 Match length 285
 % identity 87
 NCBI Description P.vulgaris mRNA for RNP1 chloroplast RNA binding protein

Seq. No. 9503
 Contig ID 16200_1.R1040
 5'-most EST LIB3170-032-Q1-K1-A4

Seq. No. 9504
 Contig ID 16200_2.R1040
 5'-most EST leu701157014.h1

Seq. No. 9505
 Contig ID 16201_1.R1040
 5'-most EST LIB3170-077-Q1-K1-F12
 Method BLASTX
 NCBI GI g404690
 BLAST score 1290
 E value 1.0e-142
 Match length 484
 % identity 51
 NCBI Description (L19075) cytochrome P450 [Catharanthus roseus]

Seq. No. 9506

Contig ID 16201_3.R1040
 5'-most EST seb700653537.h1
 Method BLASTX
 NCBI GI g4376203
 BLAST score 210
 E value 9.0e-17
 Match length 77
 % identity 47
 NCBI Description (U35226) putative cytochrome P-450 [Nicotiana
 plumbaginifolia]

Seq. No. 9507
 Contig ID 16204_1.R1040
 5'-most EST ncj700981150.h1
 Method BLASTX
 NCBI GI g3687235
 BLAST score 560
 E value 3.0e-57
 Match length 149
 % identity 75
 NCBI Description (AC005169) putative copia-like transposable element
 [Arabidopsis thaliana]

Seq. No. 9508
 Contig ID 16204_2.R1040
 5'-most EST uC-gmrominsoy206f05b1
 Method BLASTX
 NCBI GI g3687235
 BLAST score 382
 E value 1.0e-36
 Match length 116
 % identity 68
 NCBI Description (AC005169) putative copia-like transposable element
 [Arabidopsis thaliana]

Seq. No. 9509
 Contig ID 16204_3.R1040
 5'-most EST crh700854648.h1
 Method BLASTX
 NCBI GI g3687235
 BLAST score 145
 E value 3.0e-09
 Match length 44
 % identity 64
 NCBI Description (AC005169) putative copia-like transposable element
 [Arabidopsis thaliana]

Seq. No. 9510
 Contig ID 16208_1.R1040
 5'-most EST LIB3170-078-Q1-K1-D8
 Method BLASTX
 NCBI GI g1483150
 BLAST score 450
 E value 1.0e-44
 Match length 109
 % identity 78
 NCBI Description (D84417) monodehydroascorbate reductase [Arabidopsis]

068405 : 70100

```
Seq. No.          9515
Contig ID         16228_1.R1040
5'-most EST      sat701012934.h1
Method           BLASTX
NCBI GI          g2190550
BLAST score      1063
E value          1.0e-116
Match length     274
% identity       75
NCBI Description  (AC001229) ESTs gb T45673,gb N37512 come from this gene.
```


0963-4356

Seq. No.	9521
Contig ID	16253_1.R1040
5'-most EST	LIB3049-004-Q1-E1-H3

Seq. No. 9522
 Contig ID 16264_1.R1040
 5'-most EST LIB3106-093-Q1-K1-G8
 Method BLASTX
 NCBI GI g2880049
 BLAST score 235
 E value 1.0e-19
 Match length 91
 % identity 55
 NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 9523
 Contig ID 16268_1.R1040
 5'-most EST LIB3170-067-Q1-K1-G10
 Method BLASTX
 NCBI GI g1174867
 BLAST score 334
 E value 5.0e-31
 Match length 72
 % identity 85
 NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2 KD PROTEIN) >gi_633687_emb_CAA55862_(X79275) ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi_1094912_prf_2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]

Seq. No. 9524
 Contig ID 16268_2.R1040
 5'-most EST hrw701060207.h1
 Method BLASTX
 NCBI GI g1174867
 BLAST score 267
 E value 2.0e-23
 Match length 67
 % identity 78
 NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2 KD PROTEIN) >gi_633687_emb_CAA55862_(X79275) ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi_1094912_prf_2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]

Seq. No. 9525
 Contig ID 16270_1.R1040
 5'-most EST LIB3106-069-P1-K1-G3
 Method BLASTX
 NCBI GI g2104536
 BLAST score 318
 E value 3.0e-29
 Match length 120
 % identity 53
 NCBI Description (AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No. 9526


```
Contig ID      16272_1.R1040
5'-most EST   LIB3170-028-Q1-K1-E3
Method        BLASTX
NCBI GI       g1684851
BLAST score    265
E value       5.0e-24
Match length   91
% identity     64
NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]
```

```
Seq. No.          9527
Contig ID         16288_1.R1040
5'-most EST      LIB3170-030-Q1-K1-G6
Method           BLASTX
NCBI GI          g3123349
BLAST score       295
E value          1.0e-26
Match length      74
% identity        77
NCBI Description  (AJ005788) hypothetical protein [Cicer arietinum]
```

Seq. No.	9528
Contig ID	16293_1.R1040
5'-most EST	LIB3170-029-Q1-K1-B2
Method	BLASTN
NCBI GI	g4220468
BLAST score	45
E value	5.0e-16
Match length	113
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T8011 genomic sequence, complete sequence [Arabidopsis thaliana]

```
Seq. No.          9529
Contig ID         16301_1.R1040
5'-most EST      LIB3049-035-Q1-E1-H6
Method            BLASTX
NCBI GI           g4335745
BLAST score       200
E value           2.0e-15
Match length      86
% identity        50
NCBI Description   (AC006284) putative hydrolase (contains an
                  esterase/lipase/thioesterase active site serine domain
                  (prosite: PS50187) [Arabidopsis thaliana])
```

Seq. No.	9530
Contig ID	16304_1.R1040
5'-most EST	uC-qmrominsoy071d08b1

Seq. No.	9531
Contig ID	16304_2.R1040
5'-most EST	jC-qmf102220057a02a1

Seq. No.	9532
Contig ID	16312_1.R1040
5'-most EST	leu701157523.h1

09634016-101000

Method BLASTX
NCBI GI g170131
BLAST score 352
E value 3.0e-33
Match length 88
% identity 76
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No. 9533
Contig ID 16317_1.R1040
5'-most EST LIB3170-029-Q1-K1-C1

Seq. No. 9534
Contig ID 16321_1.R1040
5'-most EST LIB3049-035-Q1-E1-F9

Seq. No. 9535
Contig ID 16324_1.R1040
5'-most EST LIB3073-021-Q1-K1-F12
Method BLASTX
NCBI GI g2190548
BLAST score 244
E value 2.0e-20
Match length 68
% identity 66
NCBI Description (AC001229) EST gb_ATTS1121 comes from this gene.
[Arabidopsis thaliana]

Seq. No. 9536
Contig ID 16324_2.R1040
5'-most EST LIB3073-021-Q1-K1-F11
Method BLASTX
NCBI GI g2190548
BLAST score 359
E value 5.0e-34
Match length 106
% identity 62
NCBI Description (AC001229) EST gb_ATTS1121 comes from this gene.
[Arabidopsis thaliana]

Seq. No. 9537
Contig ID 16328_1.R1040
5'-most EST jC-gmst02400007d01a1

Seq. No. 9538
Contig ID 16335_2.R1040
5'-most EST awf700841716.h1

Seq. No. 9539
Contig ID 16337_1.R1040
5'-most EST LIB3170-031-Q1-K1-A5
Method BLASTX
NCBI GI g1588365
BLAST score 185
E value 1.0e-13
Match length 74
% identity 46

000001070498

Seq. No.	9541
Contig ID	16346_1.R1040
5'-most EST	LIB3049-035-O1-E1-E12

Method	BLASTX
NCBI GI	g4510363
BLAST score	623
E value	1.0e-64

Seq. No.	9543
Contig ID	16355_2.R1040
5'-most EST	uC-qmropic022c11b1

Seq. No.	9544
Contig ID	16355_3.R1040
5'-most EST	trc700565054.h1

Seq. No.	9545
Contig ID	16355_4.R1040
5'-most EST	trc700565456.h1

1692

09684016-101000

```
% identity          50
NCBI Description    (AC006284) putative beta-1,3-endoglucanase [Arabidopsis
                    thaliana]

Seq. No.           9558
Contig ID          16398_2.R1040
5'-most EST       LIB3050-008-Q1-E1-B3
Method            BLASTX
NCBI GI            g4335750
BLAST score        219
E value           1.0e-17
Match length       64
% identity         56
NCBI Description    (AC006284) putative beta-1,3-endoglucanase [Arabidopsis
                    thaliana]

Seq. No.           9559
Contig ID          16403_1.R1040
5'-most EST       LIB3072-049-Q1-K1-E7

Seq. No.           9560
Contig ID          16406_1.R1040
5'-most EST       uC-gmropic106g10b1

Seq. No.           9561
Contig ID          16407_1.R1040
5'-most EST       LIB3109-007-Q1-K1-D8
Method            BLASTX
NCBI GI            g1170089
BLAST score        637
E value           3.0e-66
Match length       212
% identity         57
NCBI Description    GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
                    >gi_481822_pir_S39542 probable glutathione transferase (EC
                    2.5.1.18) (clone ERD13) - Arabidopsis thaliana
                    >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase
                    [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione
                    S-transferase [Arabidopsis thaliana]

Seq. No.           9562
Contig ID          16407_2.R1040
5'-most EST       g4302960
Method            BLASTX
NCBI GI            g3201613
BLAST score        361
E value           5.0e-34
Match length       130
% identity         55
NCBI Description    (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.           9563
Contig ID          16410_1.R1040
5'-most EST       seb700650214.h1

Seq. No.           9564
Contig ID          16410_2.R1040
```


09684016-101000

5'-most EST LIB3170-029-Q1-K1-G6

Seq. No. 9565
 Contig ID 16414_1.R1040
 5'-most EST jex700908176.h1
 Method BLASTX
 NCBI GI g3738297
 BLAST score 201
 E value 1.0e-15
 Match length 67
 % identity 24
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 9566
 Contig ID 16415_1.R1040
 5'-most EST LIB3049-034-Q1-E1-E5

Seq. No. 9567
 Contig ID 16422_1.R1040
 5'-most EST sat701007849.h1
 Method BLASTX
 NCBI GI g3955021
 BLAST score 304
 E value 1.0e-27
 Match length 72
 % identity 78
 NCBI Description (AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]

Seq. No. 9568
 Contig ID 16425_1.R1040
 5'-most EST LIB3049-034-Q1-E1-C10
 Method BLASTX
 NCBI GI g3080398
 BLAST score 246
 E value 6.0e-21
 Match length 112
 % identity 24
 NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 9569
 Contig ID 16426_1.R1040
 5'-most EST uC-gmronoir007b08b1

Seq. No. 9570
 Contig ID 16426_2.R1040
 5'-most EST asn701138153.h1

Seq. No. 9571
 Contig ID 16428_1.R1040
 5'-most EST awf700836372.h1
 Method BLASTX
 NCBI GI g2959370
 BLAST score 318
 E value 8.0e-29
 Match length 139
 % identity 40

Seq. No. 9594
 Contig ID 16509_2.R1040
 5'-most EST LIB3049-028-Q1-E1-C8
 Method BLASTX
 NCBI GI g3080439
 BLAST score 356
 E value 7.0e-34
 Match length 96
 % identity 73
 NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 9595
 Contig ID 16513_1.R1040
 5'-most EST gsv701056187.h1

Seq. No. 9596
 Contig ID 16519_1.R1040
 5'-most EST LIB3049-033-Q1-E1-C7

Seq. No. 9597
 Contig ID 16525_1.R1040
 5'-most EST LIB3170-029-Q1-K1-F5

Seq. No. 9598
 Contig ID 16527_1.R1040
 5'-most EST pxt700941561.h1

Seq. No. 9599
 Contig ID 16531_2.R1040
 5'-most EST jsh701064262.h1

Seq. No. 9600
 Contig ID 16531_3.R1040
 5'-most EST LIB3065-014-Q1-N1-A7

Seq. No. 9601
 Contig ID 16531_4.R1040
 5'-most EST LIB3049-003-Q1-E1-A10
 Method BLASTN
 NCBI GI g498704
 BLAST score 33
 E value 7.0e-09
 Match length 53
 % identity 91
 NCBI Description S.oleracea slfa mRNA

Seq. No. 9602
 Contig ID 16532_1.R1040
 5'-most EST kl1701206566.h1

Seq. No. 9603
 Contig ID 16533_1.R1040
 5'-most EST LIB3049-033-Q1-E1-A6

Seq. No. 9604
 Contig ID 16547_1.R1040

SECRET

SECRET

SECRET

SECRET

SECRET

SECRET

E value 3.0e-16
 Match length 71
 % identity 54
 NCBI Description (AF060862) unknown [Homo sapiens]

Seq. No. 9619
 Contig ID 16593_1.R1040
 5'-most EST LIB3170-029-Q1-K1-B5

Seq. No. 9620
 Contig ID 16610_1.R1040
 5'-most EST LIB3051-058-Q1-K2-G8
 Method BLASTX
 NCBI GI g2833469
 BLAST score 143
 E value 1.0e-08
 Match length 119
 % identity 32
 NCBI Description HYPOTHETICAL 22.2 KD PROTEIN SLR0305
 >gi_1001792_dbj_BAA10672_ (D64005) hypothetical protein
 [Synechocystis sp.]

Seq. No. 9621
 Contig ID 16631_1.R1040
 5'-most EST LIB3139-094-P1-N1-E8
 Method BLASTX
 NCBI GI g4559384
 BLAST score 924
 E value 1.0e-100
 Match length 244
 % identity 73
 NCBI Description (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No. 9622
 Contig ID 16631_2.R1040
 5'-most EST g5509744

Seq. No. 9623
 Contig ID 16631_3.R1040
 5'-most EST wrg700787781.h2

Seq. No. 9624
 Contig ID 16637_1.R1040
 5'-most EST asn701133352.h1

Seq. No. 9625
 Contig ID 16640_1.R1040
 5'-most EST LIB3049-031-Q1-E1-G3

Seq. No. 9626
 Contig ID 16644_1.R1040
 5'-most EST wvk700681309.h2
 Method BLASTX
 NCBI GI g3510261
 BLAST score 397
 E value 2.0e-38
 Match length 127

% identity 58
NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No. 9627
Contig ID 16644_2.R1040
5'-most EST jC-gmro02910016f10a1
Method BLASTX
NCBI GI g3522950
BLAST score 292
E value 2.0e-26
Match length 99
% identity 62
NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 9628
Contig ID 16648_1.R1040
5'-most EST LIB3049-031-Q1-E1-D8

Seq. No. 9629
Contig ID 16649_1.R1040
5'-most EST k11701213122.h1

Seq. No. 9630
Contig ID 16655_1.R1040
5'-most EST bth700847436.h1

Seq. No. 9631
Contig ID 16656_1.R1040
5'-most EST LIB3049-031-Q1-E1-E6
Method BLASTX
NCBI GI g4558564
BLAST score 284
E value 2.0e-25
Match length 129
% identity 48
NCBI Description (AC007138) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No. 9632
Contig ID 16657_1.R1040
5'-most EST LIB3093-001-Q1-K1-F1

Seq. No. 9633
Contig ID 16660_1.R1040
5'-most EST LIB3107-030-Q1-K1-H10
Method BLASTX
NCBI GI g3193296
BLAST score 163
E value 5.0e-11
Match length 119
% identity 34
NCBI Description (AF069298) similar to pectinesterase [Arabidopsis thaliana]

Seq. No. 9634
Contig ID 16664_1.R1040
5'-most EST LIB3049-031-Q1-E1-F12

BLAST score 954
 E value 1.0e-103
 Match length 229
 % identity 77
 NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 9651
 Contig ID 16727_1.R1040
 5'-most EST LIB3109-043-Q1-K1-F12
 Method BLASTX
 NCBI GI g4455287
 BLAST score 380
 E value 2.0e-36
 Match length 140
 % identity 54
 NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 9652
 Contig ID 16727_3.R1040
 5'-most EST hrw701058080.h1

Seq. No. 9653
 Contig ID 16732_1.R1040
 5'-most EST LIB3170-030-Q1-K1-E1
 Method BLASTX
 NCBI GI g2618689
 BLAST score 545
 E value 4.0e-56
 Match length 108
 % identity 94
 NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 9654
 Contig ID 16746_1.R1040
 5'-most EST uC-gmropic023f01b1
 Method BLASTX
 NCBI GI g3046695
 BLAST score 284
 E value 1.0e-24
 Match length 136
 % identity 49
 NCBI Description (AL022224) putative protein [Arabidopsis thaliana]

Seq. No. 9655
 Contig ID 16746_2.R1040
 5'-most EST LIB3056-001-Q1-B1-H4

Seq. No. 9656
 Contig ID 16746_3.R1040
 5'-most EST LIB3094-038-Q1-K1-F3
 Method BLASTX
 NCBI GI g3046695
 BLAST score 223
 E value 7.0e-18
 Match length 135
 % identity 33
 NCBI Description (AL022224) putative protein [Arabidopsis thaliana]

09684015 10100

09684015 10100

09684015 10100

09684015 10100

09684015 10100

09684015 10100

09684015 10100

Contig ID 16772_1.R1040
5'-most EST ary700764475.h1
Method BLASTX
NCBI GI g4262226
BLAST score 249
E value 4.0e-21
Match length 86
% identity 56
NCBI Description (AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No. 9664
Contig ID 16772_2.R1040
5'-most EST jC-gmro02910007b02a1
Method BLASTX
NCBI GI g4262226
BLAST score 244
E value 1.0e-20
Match length 83
% identity 58
NCBI Description (AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No. 9665
Contig ID 16779_1.R1040
5'-most EST dpv701100971.h1
Method BLASTX
NCBI GI g2160180
BLAST score 567
E value 2.0e-58
Match length 158
% identity 66
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 9666
Contig ID 16783_2.R1040
5'-most EST LIB3139-117-P1-N1-G6
Method BLASTX
NCBI GI g3367576
BLAST score 515
E value 1.0e-51
Match length 145
% identity 67
NCBI Description (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No. 9667
Contig ID 16783_5.R1040
5'-most EST fC-gmle700557414r2

Seq. No. 9668
Contig ID 16783_6.R1040
5'-most EST hyd700727566.h1
Method BLASTX
NCBI GI g3367576
BLAST score 781
E value 9.0e-83
Match length 475
% identity 41
NCBI Description (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No. 9679
 Contig ID 16815_2.R1040
 5'-most EST hyd700726431.h1
 Method BLASTX
 NCBI GI g1168750
 BLAST score 206
 E value 5.0e-16
 Match length 121
 % identity 40
 NCBI Description CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) >gi_458230 (U04380) calcineurin B [Naegleria gruberi]

Seq. No. 9680
 Contig ID 16816_1.R1040
 5'-most EST zzp700835437.h1
 Method BLASTX
 NCBI GI g2673920
 BLAST score 287
 E value 1.0e-25
 Match length 70
 % identity 80
 NCBI Description (AC002561) similar to Drosophila couch potato protein [Arabidopsis thaliana]

Seq. No. 9681
 Contig ID 16817_1.R1040
 5'-most EST LIB3170-020-Q1-K1-A7

Seq. No. 9682
 Contig ID 16820_1.R1040
 5'-most EST LIB3049-029-Q1-E1-E3

Seq. No. 9683
 Contig ID 16822_1.R1040
 5'-most EST jC-gm1e01810009h10a1
 Method BLASTX
 NCBI GI g4454020
 BLAST score 448
 E value 3.0e-44
 Match length 154
 % identity 63
 NCBI Description (AL035396) putative protein [Arabidopsis thaliana]

Seq. No. 9684
 Contig ID 16826_1.R1040
 5'-most EST LIB3049-029-Q1-E1-F1

Seq. No. 9685
 Contig ID 16828_1.R1040
 5'-most EST LIB3170-026-Q1-K1-B12
 Method BLASTX
 NCBI GI g4335764
 BLAST score 443
 E value 1.0e-43
 Match length 207
 % identity 37

NCBI Description (AC006284) putative WRKY DNA-binding protein [Arabidopsis thaliana]

Seq. No. 9686
Contig ID 16830_1.R1040
5'-most EST leu701152566.h1
Method BLASTX
NCBI GI g3482967
BLAST score 659
E value 4.0e-69
Match length 154
% identity 77

NCBI Description (AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 9687
Contig ID 16830_2.R1040
5'-most EST LIB3049-029-Q1-E1-C12
Method BLASTX
NCBI GI g3482967
BLAST score 456
E value 2.0e-45
Match length 114
% identity 75

NCBI Description (AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 9688
Contig ID 16830_4.R1040
5'-most EST kl1701213354.h1
Method BLASTX
NCBI GI g3482967
BLAST score 276
E value 2.0e-24
Match length 67
% identity 81

NCBI Description (AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 9689
Contig ID 16836_1.R1040
5'-most EST leu701153534.h1
Method BLASTX
NCBI GI g4508078
BLAST score 470
E value 5.0e-47
Match length 96
% identity 89

NCBI Description (AC005882) 64134 [Arabidopsis thaliana]

Seq. No. 9690
Contig ID 16836_2.R1040
5'-most EST LIB3107-013-Q1-K1-D12
Method BLASTX

Contig ID 16897_1.R1040
 5'-most EST sat701009333.h1
 Method BLASTX
 NCBI GI g629623
 BLAST score 155
 E value 3.0e-10
 Match length 70
 % identity 50
 NCBI Description chalcone reductase - alfalfa >gi_563538_emb_CAA57784_ (X82368) chalcone reductase [Medicago sativa]

Seq. No. 9715
 Contig ID 16898_1.R1040
 5'-most EST ncj700983652.h1
 Method BLASTX
 NCBI GI g4151319
 BLAST score 892
 E value 2.0e-96
 Match length 250
 % identity 73
 NCBI Description (AF089084) putative auxin efflux carrier protein; AtPIN1 [Arabidopsis thaliana]

Seq. No. 9716
 Contig ID 16900_1.R1040
 5'-most EST zzp700834260.h1
 Method BLASTX
 NCBI GI g927428
 BLAST score 515
 E value 3.0e-52
 Match length 148
 % identity 68
 NCBI Description (X86733) fis1 [Linum usitatissimum]

Seq. No. 9717
 Contig ID 16902_1.R1040
 5'-most EST LIB3051-074-Q1-K1-H2
 Method BLASTX
 NCBI GI g2853097
 BLAST score 212
 E value 6.0e-17
 Match length 86
 % identity 48
 NCBI Description (AL021767) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 9718
 Contig ID 16902_2.R1040
 5'-most EST LIB3139-049-P1-N1-B7
 Method BLASTX
 NCBI GI g2853097
 BLAST score 236
 E value 2.0e-19
 Match length 142
 % identity 38
 NCBI Description (AL021767) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 9719

Seq. No. 9729
 Contig ID 16930_2.R1040
 5'-most EST LIB3049-028-Q1-E1-B7
 Method BLASTN
 NCBI GI g2160155
 BLAST score 71
 E value 1.0e-31
 Match length 171
 % identity 85
 NCBI Description Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 9730
 Contig ID 16933_1.R1040
 5'-most EST LIB3049-028-Q1-E1-A11
 Method BLASTX
 NCBI GI g3021513
 BLAST score 703
 E value 3.0e-74
 Match length 189
 % identity 72
 NCBI Description (X96728) isocitrate dehydrogenase (NADP+) [Nicotiana tabacum]

Seq. No. 9731
 Contig ID 16937_1.R1040
 5'-most EST gsv701055145.h1

Seq. No. 9732
 Contig ID 16939_1.R1040
 5'-most EST seb700651907.h1
 Method BLASTX
 NCBI GI g1903021
 BLAST score 510
 E value 1.0e-51
 Match length 125
 % identity 79
 NCBI Description (Y10216) hypothetical 3-isopropylmalate dehydrogenase [Arabidopsis thaliana]

Seq. No. 9733
 Contig ID 16939_2.R1040
 5'-most EST LIB3049-028-Q1-E1-A8
 Method BLASTX
 NCBI GI g1903021
 BLAST score 545
 E value 8.0e-56
 Match length 178
 % identity 62
 NCBI Description (Y10216) hypothetical 3-isopropylmalate dehydrogenase [Arabidopsis thaliana]

Seq. No. 9734
 Contig ID 16939_3.R1040
 5'-most EST LIB3049-015-Q1-E1-D6
 Method BLASTX

NCBI GI	g4415912
BLAST score	312
E value	3.0e-29
Match length	189
% identity	38
NCBI Description	(AC006282) putative protease [Arabidopsis thaliana]
Seq. No.	9762
Contig ID	17010_1.R1040
5'-most EST	LIB3049-002-Q1-E1-E1
Seq. No.	9763
Contig ID	17014_1.R1040
5'-most EST	LIB3170-040-Q1-K1-E5
Method	BLASTX
NCBI GI	g2245018
BLAST score	166
E value	2.0e-11
Match length	89
% identity	43
NCBI Description	(Z97341) unnamed protein product [Arabidopsis thaliana]
Seq. No.	9764
Contig ID	17014_2.R1040
5'-most EST	LIB3109-015-Q1-K1-A3
Method	BLASTX
NCBI GI	g3776027
BLAST score	165
E value	1.0e-18
Match length	81
% identity	60
NCBI Description	(AJ010475) RNA helicase [Arabidopsis thaliana]
Seq. No.	9765
Contig ID	17015_1.R1040
5'-most EST	LIB3049-027-Q1-E1-C3
Method	BLASTX
NCBI GI	g2583134
BLAST score	142
E value	7.0e-09
Match length	85
% identity	51
NCBI Description	(AC002387) putative proline-rich protein [Arabidopsis thaliana]
Seq. No.	9766
Contig ID	17017_1.R1040
5'-most EST	k11701211990.h1
Seq. No.	9767
Contig ID	17019_1.R1040
5'-most EST	LIB3049-026-Q1-E1-G9
Seq. No.	9768
Contig ID	17027_1.R1040
5'-most EST	LIB3049-026-Q1-E1-H9

Method BLASTX
 NCBI GI g1362162
 BLAST score 382
 E value 6.0e-37
 Match length 103
 % identity 64
 NCBI Description beta-glucosidase BGQ60 precursor - barley >gi_804656
 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No. 9821
 Contig ID 17187_1.R1040
 5'-most EST gsv701055639.h1
 Method BLASTX
 NCBI GI g3776559
 BLAST score 692
 E value 5.0e-73
 Match length 157
 % identity 83
 NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933
 cdc2 protein kinase homolog from A. thaliana BAC
 gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this
 gene. [Arabidopsis thaliana]

Seq. No. 9822
 Contig ID 17192_1.R1040
 5'-most EST LIB3138-079-P1-N1-H12
 Method BLASTX
 NCBI GI g2191187
 BLAST score 175
 E value 1.0e-12
 Match length 95
 % identity 43
 NCBI Description (AF007271) contains similarity to a DNAJ-like domain
 [Arabidopsis thaliana]

Seq. No. 9823
 Contig ID 17194_1.R1040
 5'-most EST LIB3170-026-Q1-J1-A8

Seq. No. 9824
 Contig ID 17199_1.R1040
 5'-most EST jC-gmst02400031h09d1
 Method BLASTX
 NCBI GI g2760844
 BLAST score 247
 E value 6.0e-21
 Match length 68
 % identity 68
 NCBI Description (AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No. 9825
 Contig ID 17210_1.R1040
 5'-most EST LIB3109-053-Q1-K1-H10
 Method BLASTX
 NCBI GI g4406764
 BLAST score 494
 E value 6.0e-51

5'-most EST epx701108947.h1

Seq. No. 9832
 Contig ID 17233_1.R1040
 5'-most EST uxk700669925.h1
 Method BLASTX
 NCBI GI g1175102
 BLAST score 217
 E value 3.0e-17
 Match length 187
 % identity 37
 NCBI Description HYPOTHETICAL PROTEIN HI0077 >gi_1074247_pir_G64000
 hypothetical protein HI0077 - Haemophilus influenzae
 (strain Rd KW20) >gi_1573032 (U32693) H. influenzae
 predicted coding region HI0077 [Haemophilus influenzae Rd]

Seq. No. 9833
 Contig ID 17243_1.R1040
 5'-most EST LIB3170-026-Q1-K1-F7

Seq. No. 9834
 Contig ID 17244_1.R1040
 5'-most EST LIB3049-024-Q1-E1-B6

Seq. No. 9835
 Contig ID 17248_1.R1040
 5'-most EST LIB3170-026-Q1-K1-G7

Seq. No. 9836
 Contig ID 17259_1.R1040
 5'-most EST LIB3051-107-Q1-K1-D3
 Method BLASTX
 NCBI GI g1899188
 BLAST score 301
 E value 2.0e-27
 Match length 127
 % identity 37
 NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No. 9837
 Contig ID 17259_2.R1040
 5'-most EST LIB3087-009-Q1-K1-E2
 Method BLASTX
 NCBI GI g4455223
 BLAST score 396
 E value 2.0e-38
 Match length 116
 % identity 23
 NCBI Description (AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No. 9838
 Contig ID 17259_3.R1040
 5'-most EST jC-gmro02910003f05a1
 Method BLASTX
 NCBI GI g2708532
 BLAST score 358

Seq. No. 9877
 Contig ID 17353_1.R1040
 5'-most EST hyd700729857.h1
 Method BLASTX
 NCBI GI g112785
 BLAST score 395
 E value 5.0e-38
 Match length 178
 % identity 42
 NCBI Description DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I) >gi_67508_pir__DGECM1 3-methyladenine DNA glycosylase (EC 3.2.2.-) I - Escherichia coli >gi_43030_emb_CAA27472_(X03845) TAGI (aa 1-187) [Escherichia coli] >gi_147920 (J02606) 3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] >gi_466687 (U00039) 3-methyladenine-DNA glycosylase I, constitutive [Escherichia coli] >gi_1789971 (AE000432) 3-methyl-adenine DNA glycosylase I, constitutive [Escherichia coli]

Seq. No. 9878
 Contig ID 17355_1.R1040
 5'-most EST fua701040371.h1

Seq. No. 9879
 Contig ID 17355_2.R1040
 5'-most EST jsh701067431.h1

Seq. No. 9880
 Contig ID 17356_1.R1040
 5'-most EST LIB3065-019-Q1-N1-A5
 Method BLASTX
 NCBI GI g3901012
 BLAST score 551
 E value 1.0e-113
 Match length 276
 % identity 72
 NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No. 9881
 Contig ID 17359_1.R1040
 5'-most EST LIB3049-022-Q1-E1-C8

Seq. No. 9882
 Contig ID 17364_1.R1040
 5'-most EST LIB3049-022-Q1-E1-B12
 Method BLASTX
 NCBI GI g1703190
 BLAST score 159
 E value 8.0e-11
 Match length 105
 % identity 33
 NCBI Description AF-10 PROTEIN >gi_538277 (U13948) zinc finger/leucine zipper protein [Homo sapiens]

Contig ID 17375_1.R1040
 5'-most EST uC-gmrominsoyl57h02b1
 Method BLASTX
 NCBI GI g481762
 BLAST score 162
 E value 7.0e-11
 Match length 181
 % identity 28
 NCBI Description beta-adaptin 1 - fruit fly (*Drosophila melanogaster*)
 >gi_434902_emb_CAA53509_(X75910) beta-adaptin *Drosophila* 1
 [*Drosophila melanogaster*]

Seq. No. 9890
 Contig ID 17377_1.R1040
 5'-most EST leu701144426.h1
 Method BLASTX
 NCBI GI g3746059
 BLAST score 556
 E value 4.0e-57
 Match length 151
 % identity 65
 NCBI Description (AC005311) putative cysteinyl-tRNA synthetase [*Arabidopsis thaliana*] >gi_4432812_gb_AAD20662_(AC006593) putative
 cysteinyl-tRNA synthetase [*Arabidopsis thaliana*]

Seq. No. 9891
 Contig ID 17377_2.R1040
 5'-most EST leu701152494.h1
 Method BLASTX
 NCBI GI g3746059
 BLAST score 237
 E value 1.0e-19
 Match length 105
 % identity 49
 NCBI Description (AC005311) putative cysteinyl-tRNA synthetase [*Arabidopsis thaliana*] >gi_4432812_gb_AAD20662_(AC006593) putative
 cysteinyl-tRNA synthetase [*Arabidopsis thaliana*]

Seq. No. 9892
 Contig ID 17381_1.R1040
 5'-most EST LIB3049-021-Q1-E1-H5

Seq. No. 9893
 Contig ID 17384_1.R1040
 5'-most EST LIB3049-021-Q1-E1-H8

Seq. No. 9894
 Contig ID 17385_1.R1040
 5'-most EST ncj700978967.h1

Seq. No. 9895
 Contig ID 17390_1.R1040
 5'-most EST LIB3170-028-Q1-K1-C5

Seq. No. 9896
 Contig ID 17391_1.R1040
 5'-most EST LIB3049-022-Q1-E1-A3

Seq. No. 9897
 Contig ID 17394_1.R1040
 5'-most EST zhf700953342.h1

Seq. No. 9898
 Contig ID 17399_1.R1040
 5'-most EST jC-gmle01810084a09a1
 Method BLASTX
 NCBI GI g121083
 BLAST score 3312
 E value 0.0e+00
 Match length 693
 % identity 90
 NCBI Description GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)
 >gi_282926_pir_A42109 glycine dehydrogenase
 (decarboxylating) (EC 1.4.4.2) component P precursor -
 garden pea >gi_20741_emb_CAA42443_ (X59773) component of
 aminomethyltransferase [*Pisum sativum*]

Seq. No. 9899
 Contig ID 17399_2.R1040
 5'-most EST LIB3138-016-Q1-N1-D8
 Method BLASTN
 NCBI GI g20738
 BLAST score 69
 E value 3.0e-30
 Match length 97
 % identity 93
 NCBI Description *P. sativum* gdcP gene for P-protein of glycine decarboxylase
 enzyme complex

Seq. No. 9900
 Contig ID 17399_3.R1040
 5'-most EST wrg700788492.h1
 Method BLASTN
 NCBI GI g20738
 BLAST score 197
 E value 1.0e-106
 Match length 364
 % identity 91
 NCBI Description *P. sativum* gdcP gene for P-protein of glycine decarboxylase
 enzyme complex

Seq. No. 9901
 Contig ID 17399_4.R1040
 5'-most EST g5753163
 Method BLASTN
 NCBI GI g20740
 BLAST score 154
 E value 9.0e-81
 Match length 634
 % identity 89
 NCBI Description *Pisum sativum* mRNA for P protein, a part of glycine
 cleavage complex

5'-most EST LIB3049-021-Q1-E1-E8
 Method BLASTX
 NCBI GI g2642450
 BLAST score 452
 E value 7.0e-45
 Match length 121
 % identity 74
 NCBI Description (AC002391) putative metal ion transporter (Nramp)
 [Arabidopsis thaliana] >gi_3169188 (AC004401) putative
 metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No. 9913
 Contig ID 17436_1.R1040
 5'-most EST LIB3170-026-Q1-K1-H3

Seq. No. 9914
 Contig ID 17437_1.R1040
 5'-most EST awf700840951.h1
 Method BLASTX
 NCBI GI g2088647
 BLAST score 655
 E value 1.0e-68
 Match length 171
 % identity 74
 NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]
 >gi_3158394 (AF036340) LRR-containing F-box protein
 [Arabidopsis thaliana]

Seq. No. 9915
 Contig ID 17442_1.R1040
 5'-most EST pcp700991595.h1

Seq. No. 9916
 Contig ID 17448_1.R1040
 5'-most EST LIB3049-008-Q1-E1-A11
 Method BLASTX
 NCBI GI g2500717
 BLAST score 266
 E value 3.0e-23
 Match length 124
 % identity 49
 NCBI Description STS14 PROTEIN PRECURSOR >gi_2129995_pir_S65052
 pistil-specific protein sts14 precursor - potato
 >gi_1236785_emb_CAA57976_ (X82652) sts14 [Solanum
 tuberosum] >gi_1589691_prf_2211417A sts14 gene [Solanum
 tuberosum]

Seq. No. 9917
 Contig ID 17453_1.R1040
 5'-most EST LIB3170-026-Q1-K1-F3

Seq. No. 9918
 Contig ID 17456_1.R1040
 5'-most EST LIB3049-021-Q1-E1-A4

Seq. No. 9919
 Contig ID 17457_1.R1040

BLAST score	453
E value	5.0e-45
Match length	119
% identity	76
NCBI Description	(AF051135) putative ubiquitin activating enzyme E1 [Arabidopsis thaliana]
Seq. No.	9932
Contig ID	17476_2.R1040
5'-most EST	LIB3109-005-Q1-K1-C9
Method	BLASTX
NCBI GI	g2952433
BLAST score	306
E value	6.0e-28
Match length	87
% identity	84
NCBI Description	(AF051135) putative ubiquitin activating enzyme E1 [Arabidopsis thaliana]
Seq. No.	9933
Contig ID	17478_1.R1040
5'-most EST	LIB3170-026-Q1-K1-C3
Seq. No.	9934
Contig ID	17479_1.R1040
5'-most EST	k11701207665.h1
Method	BLASTX
NCBI GI	g3695388
BLAST score	250
E value	4.0e-21
Match length	58
% identity	72
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]
Seq. No.	9935
Contig ID	17481_1.R1040
5'-most EST	pcp700989792.h1
Method	BLASTX
NCBI GI	g4101626
BLAST score	626
E value	5.0e-65
Match length	255
% identity	48
NCBI Description	(AF005096) desaturase/cytochrome b5 protein [Ricinus communis]
Seq. No.	9936
Contig ID	17483_1.R1040
5'-most EST	pmv700890620.h1
Seq. No.	9937
Contig ID	17486_1.R1040
5'-most EST	LIB3049-020-Q1-E1-H9
Method	BLASTX
NCBI GI	g3184096
BLAST score	147
E value	2.0e-09

Match length 129
 % identity 26
 NCBI Description (AL023777) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 9938
 Contig ID 17488_1.R1040
 5'-most EST LIB3170-027-Q2-K1-F3

Seq. No. 9939
 Contig ID 17492_1.R1040
 5'-most EST LIB3049-020-Q1-E1-F7
 Method BLASTX
 NCBI GI g3420047
 BLAST score 244
 E value 9.0e-21
 Match length 106
 % identity 56
 NCBI Description (AC004680) putative protein kinase [Arabidopsis thaliana]

Seq. No. 9940
 Contig ID 17494_1.R1040
 5'-most EST LIB3170-028-Q1-K1-F3

Seq. No. 9941
 Contig ID 17498_1.R1040
 5'-most EST LIB3049-020-Q1-E1-F9

Seq. No. 9942
 Contig ID 17499_1.R1040
 5'-most EST LIB3049-020-Q1-E1-G10

Seq. No. 9943
 Contig ID 17500_1.R1040
 5'-most EST LIB3049-020-Q1-E1-G11
 Method BLASTX
 NCBI GI g3269286
 BLAST score 403
 E value 5.0e-39
 Match length 132
 % identity 66
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 9944
 Contig ID 17503_1.R1040
 5'-most EST LIB3049-020-Q1-E1-G3

Seq. No. 9945
 Contig ID 17508_1.R1040
 5'-most EST jex700906877.h1
 Method BLASTN
 NCBI GI g1370171
 BLAST score 317
 E value 1.0e-178
 Match length 694
 % identity 88
 NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1X

E value	8.0e-22
Match length	172
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]
Seq. No.	9986
Contig ID	17612_1.R1040
5'-most EST	LIB3139-031-P1-N1-F7
Method	BLASTX
NCBI GI	g3367522
BLAST score	1074
E value	1.0e-117
Match length	322
% identity	64
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]
Seq. No.	9987
Contig ID	17619_1.R1040
5'-most EST	LIB3065-027-Q1-N1-B1
Method	BLASTX
NCBI GI	g1050918
BLAST score	302
E value	4.0e-27
Match length	92
% identity	60
NCBI Description	(X92648) lipid transfer protein [Helianthus annuus]
Seq. No.	9988
Contig ID	17619_2.R1040
5'-most EST	LIB3170-014-Q1-K1-G11
Method	BLASTX
NCBI GI	g3914136
BLAST score	284
E value	5.0e-25
Match length	100
% identity	56
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi_2632171_emb_CAA05771_ (AJ002958) lipid transfer protein [Cicer arietinum]
Seq. No.	9989
Contig ID	17619_3.R1040
5'-most EST	uaw700665883.h1
Method	BLASTX
NCBI GI	g2407271
BLAST score	168
E value	6.0e-12
Match length	78
% identity	49
NCBI Description	(AF017358) lipid transfer protein [Oryza sativa]
Seq. No.	9990
Contig ID	17621_1.R1040
5'-most EST	LIB3049-019-Q1-E1-C2

[illegible]

```

Seq. No.          10051
Contig ID         17827_3.R1040
5'-most EST      LIB3106-074-Q1-K1-H3
Method            BLASTN
NCBI GI           g3176071
BLAST score       165
E value           1.0e-87
Match length      332
% identity        92
NCBI Description  Medicago sativa mRNA for protein phosphatase 1, beta
                  subunit

```

```
Seq. No.          10052
Contig ID         17827_4.R1040
5'-most EST      k11701214536.h1
Method            BLASTX
NCBI GI           g3176074
BLAST score       480
E value           2.0e-48
Match length      138
% identity        70
NCBI Description  (AJ002486) protein phosphatase 1, catalytic gsmms subunit
                  [Medicago sativa]
```

```
Seq. No.          10053
Contig ID         17829_1.R1040
5'-most EST      LIB3138-034-Q1-N1-E3
Method           BLASTX
NCBI GI          g3860250
BLAST score      277
E value          2.0e-24
Match length     83
% identity       59
NCBI Description  (AC005824) putative chloroplast prephenate dehydratase
                  [Arabidopsis thaliana]
```

1767

Match length 90
 % identity 53
 NCBI Description (AC005824) putative chloroplast prephenate dehydratase
 [Arabidopsis thaliana]

Seq. No. 10055
 Contig ID 17830_1.R1040
 5'-most EST LIB3049-016-Q1-E1-E10
 Method BLASTX
 NCBI GI g1621438
 BLAST score 125
 E value 3.0e-09
 Match length 138
 % identity 30
 NCBI Description (U71603) mitochondrial transport protein amc-1 [Emericella
 nidulans]

Seq. No. 10056
 Contig ID 17832_1.R1040
 5'-most EST LIB3049-016-Q1-E1-E12
 Method BLASTX
 NCBI GI g4454480
 BLAST score 279
 E value 2.0e-24
 Match length 90
 % identity 61
 NCBI Description (AC006234) putative (1-4)-beta-mannan endohydrolase
 [Arabidopsis thaliana]

Seq. No. 10057
 Contig ID 17839_1.R1040
 5'-most EST epx701105337.h1

Seq. No. 10058
 Contig ID 17841_2.R1040
 5'-most EST jC-gm1e01810020a05d1

Seq. No. 10059
 Contig ID 17841_3.R1040
 5'-most EST LIB3049-016-Q1-E1-F10
 Method BLASTX
 NCBI GI g1174850
 BLAST score 743
 E value 9.0e-79
 Match length 149
 % identity 92
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN
 LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)

Seq. No. 10060
 Contig ID 17841_4.R1040
 5'-most EST LIB3109-047-Q1-K1-D8
 Method BLASTX
 NCBI GI g1174850
 BLAST score 753
 E value 7.0e-80
 Match length 149

% identity 93
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)

Seq. No. 10061
 Contig ID 17841 5.R1040
 5'-most EST sat701006343.h1
 Method BLASTX
 NCBI GI g431270
 BLAST score 390
 E value 1.0e-37
 Match length 80
 % identity 89
 NCBI Description (L19356) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No. 10062
 Contig ID 17841 6.R1040
 5'-most EST zhf700954546.h1
 Method BLASTX
 NCBI GI g136644
 BLAST score 202
 E value 5.0e-16
 Match length 42
 % identity 88
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_100765_pir_A34506 23K ubiquitin carrier protein E2 - wheat >gi_170782 (M28059) ubiquitin carrier protein [Triticum vulgare]

Seq. No. 10063
 Contig ID 17841 7.R1040
 5'-most EST uC-gmronoir023h05b1
 Method BLASTN
 NCBI GI g431269
 BLAST score 46
 E value 8.0e-17
 Match length 105
 % identity 92
 NCBI Description Arabidopsis thaliana ubiquitin conjugating enzyme (UBC5) gene, complete cds

Seq. No. 10064
 Contig ID 17843 1.R1040
 5'-most EST wrg700786292.h2
 Method BLASTX
 NCBI GI g4406815
 BLAST score 731
 E value 2.0e-77
 Match length 209
 % identity 67
 NCBI Description (AC006201) putative peptide methionine sulfoxide reductase [Arabidopsis thaliana]

Seq. No. 10065
 Contig ID 17843 2.R1040
 5'-most EST LIB3170-021-Q1-K1-H2

Method BLASTX
 NCBI GI g4406815
 BLAST score 275
 E value 3.0e-24
 Match length 81
 % identity 64
 NCBI Description (AC006201) putative peptide methionine sulfoxide reductase
 [Arabidopsis thaliana]

Seq. No. 10066
 Contig ID 17845_2.R1040
 5'-most EST pxt700946337.h1
 Method BLASTX
 NCBI GI g3288888
 BLAST score 145
 E value 4.0e-09
 Match length 116
 % identity 28
 NCBI Description (AC005253) R26445_1 [Homo sapiens]

Seq. No. 10067
 Contig ID 17849_1.R1040
 5'-most EST trc700565235.h1
 Method BLASTX
 NCBI GI g4559356
 BLAST score 163
 E value 6.0e-11
 Match length 146
 % identity 10
 NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No. 10068
 Contig ID 17855_1.R1040
 5'-most EST jC-gmst02400076f04a1
 Method BLASTX
 NCBI GI g4218121
 BLAST score 148
 E value 3.0e-09
 Match length 43
 % identity 56
 NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 10069
 Contig ID 17855_2.R1040
 5'-most EST LIB3049-016-Q1-E1-D10
 Method BLASTX
 NCBI GI g4218121
 BLAST score 413
 E value 3.0e-40
 Match length 152
 % identity 55
 NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 10070
 Contig ID 17856_1.R1040
 5'-most EST LIB3107-035-Q1-K1-E9
 Method BLASTX

NCBI GI g4206210
 BLAST score 336
 E value 2.0e-31
 Match length 128
 % identity 54
 NCBI Description (AF071527) putative calcium channel [Arabidopsis thaliana]
 >gi_4263043_gb_AAD15312_ (AC005142) putative calcium
 channel [Arabidopsis thaliana]

Seq. No. 10071
 Contig ID 17860_1.R1040
 5'-most EST LIB3049-016-Q1-E1-D5

Seq. No. 10072
 Contig ID 17861_1.R1040
 5'-most EST LIB3049-016-Q1-E1-D6

Seq. No. 10073
 Contig ID 17863_1.R1040
 5'-most EST vzy700755952.h1
 Method BLASTX
 NCBI GI g465820
 BLAST score 587
 E value 1.0e-60
 Match length 161
 % identity 63
 NCBI Description HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III
 >gi_280536_pir_S28301 hypothetical protein C40H1.6 -
 Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154)
 C40H1.6 [Caenorhabditis elegans]

Seq. No. 10074
 Contig ID 17868_1.R1040
 5'-most EST leu701156625.h1
 Method BLASTX
 NCBI GI g3860273
 BLAST score 172
 E value 2.0e-12
 Match length 95
 % identity 45
 NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]
 >gi_4314398_gb_AAD15608_ (AC006232) hypothetical protein
 [Arabidopsis thaliana]

Seq. No. 10075
 Contig ID 17869_1.R1040
 5'-most EST LIB3170-023-Q1-K1-H5

Seq. No. 10076
 Contig ID 17881_1.R1040
 5'-most EST leu701144861.h1
 Method BLASTX
 NCBI GI g1255954
 BLAST score 490
 E value 3.0e-49
 Match length 116
 % identity 77

NCBI Description (Z70677) thioredoxin [*Ricinus communis*]

Seq. No. 10077
Contig ID 17881_2.R1040
5'-most EST jC-gmst02400004a08d1
Method BLASTX
NCBI GI g586099
BLAST score 224
E value 4.0e-18
Match length 54
% identity 78
NCBI Description THIOREDOXIN H-TYPE 2 (TRX-H2) >gi_486690_pir_S34812
thioredoxin h2 - common tobacco >gi_297519_emb_CAA77847_
(Z11803) THIOREDOXIN [*Nicotiana tabacum*]
>gi_447151_prf_1913431A thioredoxin [*Nicotiana tabacum*]

Seq. No. 10078
Contig ID 17882_1.R1040
5'-most EST hyd700727023.h1
Method BLASTX
NCBI GI g1200205
BLAST score 347
E value 3.0e-32
Match length 124
% identity 55
NCBI Description (X95753) DAG [*Antirrhinum majus*]

Seq. No. 10079
Contig ID 17886_1.R1040
5'-most EST LIB3049-015-Q1-E1-H6

Seq. No. 10080
Contig ID 17888_1.R1040
5'-most EST uC-gmropic022f04b1
Method BLASTX
NCBI GI g2632252
BLAST score 761
E value 7.0e-81
Match length 199
% identity 70
NCBI Description (Y12464) serine/threonine kinase [*Sorghum bicolor*]

Seq. No. 10081
Contig ID 17888_2.R1040
5'-most EST kmv700740252.h1
Method BLASTX
NCBI GI g3885328
BLAST score 1525
E value 1.0e-170
Match length 338
% identity 83
NCBI Description (AC005623) putative serine/threonine protein kinase
[*Arabidopsis thaliana*]

Seq. No. 10082
Contig ID 17888_3.R1040
5'-most EST LIB3138-127-Q1-N1-C4

Seq. No. 10083
 Contig ID 17888_4.R1040
 5'-most EST jC-gm1e01810044e03a1

Seq. No. 10084
 Contig ID 17888_6.R1040
 5'-most EST jC-gm1e01810075e03d1
 Method BLASTX
 NCBI GI g3885328
 BLAST score 210
 E value 1.0e-16
 Match length 43
 % identity 95
 NCBI Description (AC005623) putative serine/threonine protein kinase
 [Arabidopsis thaliana]

Seq. No. 10085
 Contig ID 17888_8.R1040
 5'-most EST zzp700831282.h1
 Method BLASTX
 NCBI GI g3885328
 BLAST score 207
 E value 2.0e-16
 Match length 43
 % identity 93
 NCBI Description (AC005623) putative serine/threonine protein kinase
 [Arabidopsis thaliana]

Seq. No. 10086
 Contig ID 17889_1.R1040
 5'-most EST jC-gm1f102220138c12a1
 Method BLASTX
 NCBI GI g4220474
 BLAST score 266
 E value 5.0e-23
 Match length 92
 % identity 68
 NCBI Description (AC006069) putative myosin heavy chain [Arabidopsis
 thaliana]

Seq. No. 10087
 Contig ID 17903_1.R1040
 5'-most EST fua701043040.h1

Seq. No. 10088
 Contig ID 17903_2.R1040
 5'-most EST LIB3093-016-Q1-K1-H8

Seq. No. 10089
 Contig ID 17907_1.R1040
 5'-most EST LIB3049-015-Q1-E1-G5
 Method BLASTX
 NCBI GI g2148045
 BLAST score 165
 E value 2.0e-11
 Match length 120

% identity 30
 NCBI Description self-incompatibility protein S3 precursor - Papaver rhoeas
 >gi_1107841_emb_CAA60578_ (X87100) S3 self-incompatibility
 protein [Papaver rhoeas] >gi_1107843_emb_CAA60579_ (X87101)
 S3 self-incompatibility protein [Papaver rhoeas]

Seq. No. 10090
 Contig ID 17912_1.R1040
 5'-most EST jsh701069991.h2
 Method BLASTX
 NCBI GI g3858935
 BLAST score 652
 E value 4.0e-68
 Match length 212
 % identity 53
 NCBI Description (AL021636) synaptobrevin-like protein [Arabidopsis
 thaliana] >gi_4103357 (AF025332) vesicle-associated
 membrane protein 7C; synaptobrevin 7C [Arabidopsis
 thaliana]

Seq. No. 10091
 Contig ID 17912_2.R1040
 5'-most EST jsh701069609.h1
 Method BLASTX
 NCBI GI g3858935
 BLAST score 182
 E value 1.0e-13
 Match length 55
 % identity 58
 NCBI Description (AL021636) synaptobrevin-like protein [Arabidopsis
 thaliana] >gi_4103357 (AF025332) vesicle-associated
 membrane protein 7C; synaptobrevin 7C [Arabidopsis
 thaliana]

Seq. No. 10092
 Contig ID 17913_1.R1040
 5'-most EST LIB3170-055-Q1-K1-F2
 Method BLASTX
 NCBI GI g2315449
 BLAST score 415
 E value 3.0e-40
 Match length 231
 % identity 43
 NCBI Description (AF016448) similar to Saccharomyces cerevisiae nuclear
 protein SNF7 (SP:P39929) in one region and the chromosome
 segregation protein SMC2 (SP:P38989) in another
 [Caenorhabditis elegans]

Seq. No. 10093
 Contig ID 17913_2.R1040
 5'-most EST gsv701053216.h1
 Method BLASTX
 NCBI GI g3218396
 BLAST score 191
 E value 2.0e-14
 Match length 74
 % identity 53

NCBI Description (AL023860) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 10094
Contig ID 17921_1.R1040
5'-most EST jC-gmf102220092c07d1

Seq. No. 10095
Contig ID 17923_1.R1040
5'-most EST uC-gmrominsoy186d03b1
Method BLASTX
NCBI GI g2129698
BLAST score 780
E value 3.0e-83
Match length 184
% identity 80

NCBI Description protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
>gi_1054633_emb_CAA63387_ (X92728) protein kinase
[Arabidopsis thaliana]

Seq. No. 10096
Contig ID 17926_1.R1040
5'-most EST LIB3049-015-Q1-E1-E8

Seq. No. 10097
Contig ID 17928_1.R1040
5'-most EST pxt700941235.h1
Method BLASTX
NCBI GI g3150410
BLAST score 363
E value 5.0e-34
Match length 236
% identity 33

NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]

Seq. No. 10098
Contig ID 17928_3.R1040
5'-most EST LIB3049-015-Q1-E1-D4

Seq. No. 10099
Contig ID 17932_1.R1040
5'-most EST LIB3170-022-Q1-K1-G4

Seq. No. 10100
Contig ID 17933_1.R1040
5'-most EST LIB3049-015-Q1-E1-C12

Seq. No. 10101
Contig ID 17938_1.R1040
5'-most EST jC-gmst02400050c04a1
Method BLASTX
NCBI GI g3643603
BLAST score 1113
E value 1.0e-122
Match length 295
% identity 74

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 10102
 Contig ID 17941_1.R1040
 5'-most EST LIB3049-015-Q1-E1-D1
 Method BLASTX
 NCBI GI g2213594
 BLAST score 307
 E value 5.0e-28
 Match length 64
 % identity 81
 NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 10103
 Contig ID 17943_1.R1040
 5'-most EST epv701107744.h1
 Method BLASTX
 NCBI GI g585973
 BLAST score 179
 E value 1.0e-12
 Match length 110
 % identity 40
 NCBI Description FRUCTOKINASE >gi_626018_pir_S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283_ (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf_2108342A fructokinase [Solanum tuberosum]

Seq. No. 10104
 Contig ID 17945_1.R1040
 5'-most EST LIB3049-015-Q1-E1-D2
 Method BLASTX
 NCBI GI g4539351
 BLAST score 369
 E value 4.0e-35
 Match length 154
 % identity 50
 NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 10105
 Contig ID 17946_1.R1040
 5'-most EST uC-gmflminsoy022c08b1
 Method BLASTX
 NCBI GI g4432863
 BLAST score 179
 E value 5.0e-13
 Match length 60
 % identity 53
 NCBI Description (AC006300) putative phosphate/phosphoenolpyruvate translocator protein [Arabidopsis thaliana]

Seq. No. 10106
 Contig ID 17955_1.R1040
 5'-most EST fde700874633.h1

Seq. No. 10107
 Contig ID 17956_1.R1040
 5'-most EST gsv701053913.h1

Seq. No. 10108

Contig ID 17962_1.R1040
5'-most EST sat701011715.h1

Seq. No. 10109
Contig ID 17962_2.R1040
5'-most EST LIB3049-015-Q1-E1-B2
Method BLASTX
NCBI GI g4210451
BLAST score 150
E value 2.0e-09
Match length 57
% identity 56
NCBI Description (AB016472) ARR2 protein [Arabidopsis thaliana]

Seq. No. 10110
Contig ID 17966_1.R1040
5'-most EST uC-gmropic112d10b1
Method BLASTX
NCBI GI g2245082
BLAST score 156
E value 7.0e-10
Match length 82
% identity 41
NCBI Description (Z97343) SCARECROW homolog [Arabidopsis thaliana]

Seq. No. 10111
Contig ID 17966_2.R1040
5'-most EST LIB3170-023-Q1-K1-G5

Seq. No. 10112
Contig ID 17966_3.R1040
5'-most EST smc700747161.h1

Seq. No. 10113
Contig ID 17969_1.R1040
5'-most EST LIB3049-013-Q1-E1-D7
Method BLASTX
NCBI GI g2252628
BLAST score 183
E value 1.0e-13
Match length 57
% identity 72
NCBI Description (U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No. 10114
Contig ID 17970_1.R1040
5'-most EST uC-gmrominsoy307f04b1

Seq. No. 10115
Contig ID 17971_1.R1040
5'-most EST kll701210033.h1

Seq. No. 10116
Contig ID 17971_2.R1040
5'-most EST LIB3049-014-Q1-E1-G11

Seq. No. 10117

Contig ID 17994_1.R1040
 5'-most EST uC-gmropic070g10b1
 Method BLASTX
 NCBI GI g2435511
 BLAST score 513
 E value 1.0e-51
 Match length 190
 % identity 55
 NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase
 alpha subunit [Arabidopsis thaliana]

Seq. No. 10125
 Contig ID 17994_2.R1040
 5'-most EST leu701146423.h1
 Method BLASTX
 NCBI GI g2435511
 BLAST score 452
 E value 1.0e-46
 Match length 192
 % identity 54
 NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase
 alpha subunit [Arabidopsis thaliana]

Seq. No. 10126
 Contig ID 17997_1.R1040
 5'-most EST k11701215377.h1
 Method BLASTX
 NCBI GI g1946355
 BLAST score 487
 E value 8.0e-49
 Match length 220
 % identity 41
 NCBI Description (U93215) maize transposon MuDR mudrA protein isolog
 [Arabidopsis thaliana] >gi_2880040 (AC002340) maize
 transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 10127
 Contig ID 17999_1.R1040
 5'-most EST LIB3106-043-Q1-K1-H5

Seq. No. 10128
 Contig ID 17999_2.R1040
 5'-most EST LIB3049-014-Q1-E1-E8

Seq. No. 10129
 Contig ID 18000_1.R1040
 5'-most EST epX701107566.h1
 Method BLASTX
 NCBI GI g2494100
 BLAST score 699
 E value 1.0e-73
 Match length 259
 % identity 49
 NCBI Description NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (NADP-GDH)
 (NAD(P)H-DEPENDENT GLUTAMATE DEHYDROGENASE) >gi_1772845
 (U82240) NAD(P)H-dependent glutamate dehydrogenase
 [Prevotella ruminicola]

Match length	64
% identity	69
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.	10136
Contig ID	18022_1.R1040
5'-most EST	LIB3106-049-Q1-K1-B11
Seq. No.	10137
Contig ID	18028_1.R1040
5'-most EST	LIB3049-013-Q1-E1-H3
Seq. No.	10138
Contig ID	18031_1.R1040
5'-most EST	uC-gmflminsoy071b04b2
Method	BLASTX
NCBI GI	g2916917
BLAST score	633
E value	1.0e-80
Match length	373
% identity	44
NCBI Description	(AL022004) hypothetical protein Rv0858c [Mycobacterium tuberculosis]
Seq. No.	10139
Contig ID	18036_1.R1040
5'-most EST	LIB3049-014-Q1-E1-A11
Seq. No.	10140
Contig ID	18040_1.R1040
5'-most EST	LIB3049-014-Q1-E1-A6
Seq. No.	10141
Contig ID	18041_1.R1040
5'-most EST	crh700854610.h1
Method	BLASTX
NCBI GI	g3482974
BLAST score	1155
E value	1.0e-127
Match length	323
% identity	70
NCBI Description	(AL031369) ATP-dependent Clp proteinase-like protein [Arabidopsis thaliana]
Seq. No.	10142
Contig ID	18042_1.R1040
5'-most EST	LIB3049-014-Q1-E1-A8
Method	BLASTX
NCBI GI	g4558659
BLAST score	456
E value	2.0e-45
Match length	118
% identity	69
NCBI Description	(AC007063) unknown protein [Arabidopsis thaliana]
Seq. No.	10143
Contig ID	18047_1.R1040

5'-most EST uC-gmropic025h12b1
 Method BLASTX
 NCBI GI g984756
 BLAST score 761
 E value 1.0e-80
 Match length 396
 % identity 44
 NCBI Description (Z54153) chilling-inducible protein [Oryza sativa]

Seq. No. 10152
 Contig ID 18068_2.R1040
 5'-most EST gsv701054946.h1
 Method BLASTX
 NCBI GI g984756
 BLAST score 218
 E value 1.0e-17
 Match length 67
 % identity 58
 NCBI Description (Z54153) chilling-inducible protein [Oryza sativa]

Seq. No. 10153
 Contig ID 18068_3.R1040
 5'-most EST zhf700964316.h1
 Method BLASTX
 NCBI GI g984756
 BLAST score 333
 E value 5.0e-31
 Match length 140
 % identity 49
 NCBI Description (Z54153) chilling-inducible protein [Oryza sativa]

Seq. No. 10154
 Contig ID 18075_1.R1040
 5'-most EST jC-gmst02400025c10a1
 Method BLASTX
 NCBI GI g3420054
 BLAST score 219
 E value 1.0e-17
 Match length 125
 % identity 42
 NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]

Seq. No. 10155
 Contig ID 18076_1.R1040
 5'-most EST LIB3051-084-Q1-K1-E8

Seq. No. 10156
 Contig ID 18076_2.R1040
 5'-most EST LIB3107-080-Q1-K1-D11

Seq. No. 10157
 Contig ID 18081_1.R1040
 5'-most EST LIB3049-013-Q1-E1-C2

Seq. No. 10158
 Contig ID 18084_1.R1040
 5'-most EST LIB3052-014-Q1-N1-G9

NCBI GI g3273202
BLAST score 414
E value 2.0e-40
Match length 106
% identity 76
NCBI Description (AB010918) response reactor4 [Arabidopsis thaliana]

Seq. No. 10166
Contig ID 18103_2.R1040
5'-most EST LIB3051-068-Q1-K1-E2
Method BLASTX
NCBI GI g3273202
BLAST score 179
E value 1.0e-12
Match length 162
% identity 31
NCBI Description (AB010918) response reactor4 [Arabidopsis thaliana]

Seq. No. 10167
Contig ID 18106_1.R1040
5'-most EST LIB3170-023-Q1-K1-F8
Method BLASTN
NCBI GI g3510347
BLAST score 45
E value 4.0e-16
Match length 182
% identity 86
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No. 10168
Contig ID 18109_1.R1040
5'-most EST uaw700663343.h1

Seq. No. 10169
Contig ID 18112_1.R1040
5'-most EST LIB3049-013-Q1-E1-C1

Seq. No. 10170
Contig ID 18114_1.R1040
5'-most EST jC-gm1e01810005b01a1
Method BLASTX
NCBI GI g4006826
BLAST score 448
E value 2.0e-44
Match length 148
% identity 59
NCBI Description (AC005970) unknown protein [Arabidopsis thaliana]

Seq. No. 10171
Contig ID 18116_1.R1040
5'-most EST leu701151307.h1
Method BLASTX
NCBI GI g2645699
BLAST score 182
E value 4.0e-13
Match length 92

0000015-101000

% identity	46
NCBI Description	(AF031933) glycine-rich RNA-binding protein [Euphorbia esula]
Seq. No.	10172
Contig ID	18117_1.R1040
5'-most EST	leu701151765.h1
Seq. No.	10173
Contig ID	18122_1.R1040
5'-most EST	epx701105809.h1
Seq. No.	10174
Contig ID	18129_1.R1040
5'-most EST	LIB3049-013-Q1-E1-A12
Seq. No.	10175
Contig ID	18129_2.R1040
5'-most EST	pmv700891366.h1
Seq. No.	10176
Contig ID	18130_1.R1040
5'-most EST	kl1701205527.h1
Seq. No.	10177
Contig ID	18136_1.R1040
5'-most EST	LIB3170-022-Q1-K1-E10
Method	BLASTX
NCBI GI	g4415912
BLAST score	169
E value	6.0e-12
Match length	65
% identity	62
NCBI Description	(AC006282) putative protease [Arabidopsis thaliana]
Seq. No.	10178
Contig ID	18138_1.R1040
5'-most EST	pxt700944466.h1
Seq. No.	10179
Contig ID	18139_1.R1040
5'-most EST	LIB3170-070-Q1-K2-B6
Method	BLASTX
NCBI GI	g3763916
BLAST score	293
E value	3.0e-26
Match length	103
% identity	51
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]
Seq. No.	10180
Contig ID	18139_2.R1040
5'-most EST	hrw701061944.h1
Method	BLASTX
NCBI GI	g3763916

NCBI GI g2245101
 BLAST score 517
 E value 2.0e-52
 Match length 144
 % identity 71
 NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 10194
 Contig ID 18169_3.R1040
 5'-most EST LIB3170-022-Q1-K1-E5
 Method BLASTX
 NCBI GI g2245101
 BLAST score 332
 E value 6.0e-31
 Match length 72
 % identity 86
 NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 10195
 Contig ID 18169_4.R1040
 5'-most EST gsv701047470.h1

Seq. No. 10196
 Contig ID 18169_5.R1040
 5'-most EST eep700865796.h1
 Method BLASTX
 NCBI GI g2245101
 BLAST score 231
 E value 3.0e-19
 Match length 49
 % identity 90
 NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 10197
 Contig ID 18170_1.R1040
 5'-most EST jex700906004.h1
 Method BLASTX
 NCBI GI g1808656
 BLAST score 1381
 E value 1.0e-153
 Match length 311
 % identity 83
 NCBI Description (Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]

Seq. No. 10198
 Contig ID 18171_1.R1040
 5'-most EST LIB3049-012-Q1-E1-C10

Seq. No. 10199
 Contig ID 18179_1.R1040
 5'-most EST LIB3049-012-Q1-E1-B5

Seq. No. 10200
 Contig ID 18180_1.R1040
 5'-most EST LIB3139-094-P1-N1-H7
 Method BLASTX
 NCBI GI g128405

BLAST score 457
 E value 3.0e-45
 Match length 166
 % identity 57
 NCBI Description NODULIN 21 (N-21) >gi_99942_pir_S08632 nodulin-21 -
 soybean >gi_18694_emb_CAA34506_(X16488) nodulin-21 (AA
 1-201) [Glycine max]

Seq. No. 10201
 Contig ID 18183_1.R1040
 5'-most EST LIB3049-012-Q1-E1-A10
 Method BLASTX
 NCBI GI g3096939
 BLAST score 333
 E value 6.0e-31
 Match length 87
 % identity 72
 NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 10202
 Contig ID 18183_2.R1040
 5'-most EST leu701150481.h1
 Method BLASTN
 NCBI GI g3641835
 BLAST score 39
 E value 2.0e-12
 Match length 153
 % identity 85
 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20
 (ESSAII project)

Seq. No. 10203
 Contig ID 18188_1.R1040
 5'-most EST LIB3049-012-Q1-E1-A5

Seq. No. 10204
 Contig ID 18188_2.R1040
 5'-most EST hrw701060104.h1

Seq. No. 10205
 Contig ID 18192_1.R1040
 5'-most EST LIB3109-038-Q1-K1-A12

Seq. No. 10206
 Contig ID 18194_1.R1040
 5'-most EST LIB3056-002-Q1-B1-E5
 Method BLASTX
 NCBI GI g3327957
 BLAST score 209
 E value 3.0e-16
 Match length 91
 % identity 46
 NCBI Description (AF060490) TLS-associated protein TASR-2 [Mus musculus]
 >gi_3327976 (AF067730) TLS-associated protein TASR-2 [Homo
 sapiens]

Seq. No. 10207

5'-most EST	LIB3170-023-Q1-K1-E5
Seq. No.	10218
Contig ID	18221_1.R1040
5'-most EST	LIB3049-011-Q1-E1-F11
Seq. No.	10219
Contig ID	18223_1.R1040
5'-most EST	LIB3049-011-Q1-E1-F3
Seq. No.	10220
Contig ID	18231_1.R1040
5'-most EST	jC-gmst02400060b11a1
Method	BLASTX
NCBI GI	g4510406
BLAST score	550
E value	3.0e-56
Match length	150
% identity	68
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]
Seq. No.	10221
Contig ID	18231_2.R1040
5'-most EST	pmv700892967.h1
Method	BLASTX
NCBI GI	g3367520
BLAST score	440
E value	2.0e-47
Match length	174
% identity	60
NCBI Description	(AC004392) Similar to protein kinase APK1A, tyrosine-serine-threonine kinase gb_D12522 from A. thaliana. [Arabidopsis thaliana]
Seq. No.	10222
Contig ID	18231_3.R1040
5'-most EST	epx701104778.h1
Seq. No.	10223
Contig ID	18233_1.R1040
5'-most EST	LIB3049-011-Q1-E1-E3
Method	BLASTX
NCBI GI	g2462753
BLAST score	876
E value	1.0e-94
Match length	204
% identity	77
NCBI Description	(AC002292) putative polygalacturonase [Arabidopsis thaliana]
Seq. No.	10224
Contig ID	18236_1.R1040
5'-most EST	LIB3049-011-Q1-E1-C6
Seq. No.	10225
Contig ID	18238_1.R1040
5'-most EST	uC-qmflminsoy055f12b1


```

% identity      58
NCBI Description (AC003000) unknown protein [Arabidopsis thaliana]
>gi_3790595 (AF079186) RING-H2 finger protein RHC2a
[Arabidopsis thaliana]

Seq. No.       10242
Contig ID      18267_2.R1040
5'-most EST    zzp700832279.h1

Seq. No.       10243
Contig ID      18267_3.R1040
5'-most EST    zpv700757039.h1

Seq. No.       10244
Contig ID      18271_1.R1040
5'-most EST    gsv701051833.h1
Method         BLASTX
NCBI GI        g2952433
BLAST score    625
E value        2.0e-65
Match length   146
% identity     75
NCBI Description (AF051135) putative ubiquitin activating enzyme E1
[Arabidopsis thaliana]

Seq. No.       10245
Contig ID      18272_1.R1040
5'-most EST    LIB3049-010-Q1-E1-H4
Method         BLASTX
NCBI GI        g2980782
BLAST score    228
E value        1.0e-18
Match length   141
% identity     44
NCBI Description (AL022198) hypothetical protein [Arabidopsis thaliana]

Seq. No.       10246
Contig ID      18290_1.R1040
5'-most EST    wvk700680196.h2
Method         BLASTX
NCBI GI        g3979937
BLAST score    154
E value        4.0e-10
Match length   67
% identity     43
NCBI Description (AL034393) predicted using Genefinder; cDNA EST EMBL:D65716
comes from this gene; cDNA EST yk263b1.3 comes from this
gene; cDNA EST yk263b1.5 comes from this gene; cDNA EST
EMBL:D69251 comes from this gene [Caenorhabditis elegans]

Seq. No.       10247
Contig ID      18291_1.R1040
5'-most EST    LIB3170-021-Q1-K1-D12

Seq. No.       10248
Contig ID      18293_1.R1040
5'-most EST    LIB3170-022-Q1-K1-D12

```


0-9

```
Seq. No.          10259
Contig ID         18325_1.R1040
5'-most EST      LIB3093-023-Q1-K1-D10
Method            BLASTX
NCBI GI           g3212866
BLAST score       430
E value           8.0e-42
Match length      267
% identity        37
NCBI Description  (AC004005) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.          10261
Contig ID         18333_1.R1040
5'-most EST      leu701146986.h1
Method            BLASTX
NCBI GI           g3738331
BLAST score       322
E value           9.0e-30
Match length      72
% identity        74
NCBI Description  (AC005170) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.          10262
Contig ID         18340_1.R1040
5'-most EST      k11701208052.h1
Method            BLASTX
NCBI GI           g1176658
BLAST score       227
E value           3.0e-18
Match length      80
% identity        53
NCBI Description  HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
                  >gi_726363 (U23168) No definition line found
                  [Caenorhabditis elegans]
```

Seq. No. 10264

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 10278
Contig ID 18378_1.R1040
5'-most EST LIB3049-009-Q1-E1-G10

Seq. No. 10279
Contig ID 18380_1.R1040
5'-most EST LIB3049-009-Q1-E1-G12

Seq. No. 10280
Contig ID 18387_1.R1040
5'-most EST LIB3049-009-Q1-E1-D4

Seq. No. 10281
Contig ID 18389_1.R1040
5'-most EST vzy700754587.h1
Method BLASTX
NCBI GI g3559811
BLAST score 1491
E value 1.0e-166
Match length 401
% identity 69
NCBI Description (AJ010735) gr1-protein [Arabidopsis thaliana]

Seq. No. 10282
Contig ID 18390_1.R1040
5'-most EST LIB3065-006-Q1-N1-H12
Method BLASTX
NCBI GI g416922
BLAST score 348
E value 7.0e-33
Match length 96
% identity 76
NCBI Description DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE)
(DUTP PYROPHOSPHATASE) (P18) >gi_282947_pir__JQ1599 dUTP
pyrophosphatase (EC 3.6.1.23) - tomato
>gi_251897_bbs_109276 (S40549) deoxyuridine triphosphatase,
dUTPase, P18 {EC 3.6.1.23} [tomatoes, Tint Tim cultivar
LA154, Peptide, 169 aa] [Lycopersicon esculentum]

Seq. No. 10283
Contig ID 18391_1.R1040
5'-most EST LIB3049-009-Q1-E1-D8
Method BLASTX
NCBI GI g3142297
BLAST score 363
E value 1.0e-34
Match length 96
% identity 74
NCBI Description (AC002411) Contains similarity to serine/threonine protein
phosphatase gb_X83099 from S. cerevisiae. [Arabidopsis
thaliana]

Seq. No. 10284
Contig ID 18395_1.R1040
5'-most EST LIB3170-022-Q1-K1-D1

0584016-101000

0584016-101000

0584016-101000

0584016-101000

0584016-101000

0584016-101000

0584016-101000

0584016-101000

0584016-101000

Method BLASTX
 NCBI GI g3850063
 BLAST score 787
 E value 1.0e-83
 Match length 482
 % identity 35
 NCBI Description (AJ223830) ARE1 [Rattus norvegicus]

Seq. No. 10314
 Contig ID 18478_1.R1040
 5'-most EST LIB3170-024-Q1-J1-D1
 Method BLASTX
 NCBI GI g3834322
 BLAST score 180
 E value 4.0e-13
 Match length 46
 % identity 80
 NCBI Description (AC005679) EST gb_R30300 comes from this gene. [Arabidopsis thaliana]

Seq. No. 10315
 Contig ID 18481_1.R1040
 5'-most EST LIB3170-022-Q1-K1-C11
 Method BLASTX
 NCBI GI g3080412
 BLAST score 209
 E value 3.0e-16
 Match length 129
 % identity 33
 NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 10316
 Contig ID 18486_1.R1040
 5'-most EST jC-gmfl02220148c03a1
 Method BLASTX
 NCBI GI g2289003
 BLAST score 414
 E value 2.0e-40
 Match length 129
 % identity 67
 NCBI Description (AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No. 10317
 Contig ID 18488_1.R1040
 5'-most EST LIB3056-004-Q1-N1-B2

Seq. No. 10318
 Contig ID 18489_1.R1040
 5'-most EST LIB3092-043-Q1-K1-E6
 Method BLASTX
 NCBI GI g4519673
 BLAST score 1106
 E value 1.0e-121
 Match length 280
 % identity 71
 NCBI Description (AB017694) WREBP-2 [Nicotiana tabacum]

Match length	120
% identity	71
NCBI Description	(AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana]
Seq. No.	10342
Contig ID	18549_1.R1040
5'-most EST	g5058258
Seq. No.	10343
Contig ID	18549_2.R1040
5'-most EST	jC-gmst02400061a04a1
Seq. No.	10344
Contig ID	18549_3.R1040
5'-most EST	jC-gmro02910075f07a1
Seq. No.	10345
Contig ID	18549_4.R1040
5'-most EST	leu701149641.h1
Method	BLASTX
NCBI GI	g3095111
BLAST score	193
E value	2.0e-14
Match length	144
% identity	33
NCBI Description	(AF051894) 15 kDa selenoprotein [Homo sapiens]
Seq. No.	10346
Contig ID	18560_1.R1040
5'-most EST	uC-gmrominsoyl12f04b1
Method	BLASTX
NCBI GI	g3757515
BLAST score	168
E value	2.0e-11
Match length	82
% identity	41
NCBI Description	(AC005167) hypothetical protein [Arabidopsis thaliana]
Seq. No.	10347
Contig ID	18566_1.R1040
5'-most EST	LIB3049-007-Q1-E1-A8
Seq. No.	10348
Contig ID	18567_1.R1040
5'-most EST	LIB3170-023-Q1-J1-C12
Seq. No.	10349
Contig ID	18569_1.R1040
5'-most EST	LIB3093-013-Q1-K1-F1
Seq. No.	10350
Contig ID	18572_1.R1040
5'-most EST	LIB3050-023-Q1-K1-A8
Method	BLASTX
NCBI GI	g3237190
BLAST score	237


```

E value                2.0e-19
Match length           92
% identity             51
NCBI Description       (AB014760) cystein proteinase inhibitor [Cucumis sativus]

Seq. No.               10351
Contig ID              18578_1.R1040
5'-most EST            LIB3109-006-Q1-K1-B8

Seq. No.               10352
Contig ID              18583_1.R1040
5'-most EST            jC-gmfl02220068h02d1

Seq. No.               10353
Contig ID              18585_1.R1040
5'-most EST            jC-gmfl02220102f03a1
Method                 BLASTX
NCBI GI                g542020
BLAST score            493
E value                1.0e-49
Match length           155
% identity             62
NCBI Description       sucrose transport protein - castor bean
                       >gi_468562_emb_CAA83436_ (Z31561) sucrose carrier [Ricinus
                       communis]

Seq. No.               10354
Contig ID              18586_1.R1040
5'-most EST            g4314018
Method                 BLASTX
NCBI GI                g3702343
BLAST score            1625
E value                0.0e+00
Match length           468
% identity             76
NCBI Description       (AC005397) putative homeotic gene regulator [Arabidopsis
                       thaliana]

Seq. No.               10355
Contig ID              18590_1.R1040
5'-most EST            ncj700987760.h1

Seq. No.               10356
Contig ID              18590_2.R1040
5'-most EST            kl1701214752.h1

Seq. No.               10357
Contig ID              18593_1.R1040
5'-most EST            LIB3049-006-Q1-E1-H3
Method                 BLASTX
NCBI GI                g2244765
BLAST score            285
E value                2.0e-25
Match length           94
% identity             54
NCBI Description       (Z97335) hypothetical protein [Arabidopsis thaliana]

```


% identity	90
NCBI Description	Sesbania rostrata mRNA for putative chalcone reductase
Seq. No.	10371
Contig ID	18631_1.R1040
5'-most EST	LIB3049-006-Q1-E1-E3
Method	BLASTN
NCBI GI	g169157
BLAST score	136
E value	2.0e-70
Match length	376
% identity	87
NCBI Description	Pisum sativum serine hydroxymethyltransferase mRNA, complete cds
Seq. No.	10372
Contig ID	18633_1.R1040
5'-most EST	LIB3049-006-Q1-E1-D10
Seq. No.	10373
Contig ID	18635_1.R1040
5'-most EST	zzp700832155.h1
Method	BLASTX
NCBI GI	g2213626
BLAST score	193
E value	2.0e-14
Match length	156
% identity	38
NCBI Description	(AC000103) F21J9.18 [Arabidopsis thaliana]
Seq. No.	10374
Contig ID	18635_2.R1040
5'-most EST	uaw700660817.h1
Seq. No.	10375
Contig ID	18645_1.R1040
5'-most EST	LIB3049-006-Q1-E1-C5
Method	BLASTX
NCBI GI	g2880043
BLAST score	734
E value	1.0e-77
Match length	300
% identity	46
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]
Seq. No.	10376
Contig ID	18647_1.R1040
5'-most EST	LIB3049-006-Q1-E1-C7
Seq. No.	10377
Contig ID	18648_1.R1040
5'-most EST	LIB3092-061-Q1-K1-C1
Seq. No.	10378
Contig ID	18651_1.R1040
5'-most EST	LIB3109-050-Q1-K1-G2

Seq. No. 10379
Contig ID 18652_1.R1040
5'-most EST LIB3170-023-Q1-K1-B9

Seq. No. 10380
Contig ID 18656_1.R1040
5'-most EST LIB3049-006-Q1-E1-A3
Method BLASTX
NCBI GI g3548801
BLAST score 346
E value 3.0e-32
Match length 192
% identity 36
NCBI Description (AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No. 10381
Contig ID 18656_2.R1040
5'-most EST leu701147073.h1
Method BLASTX
NCBI GI g3461828
BLAST score 157
E value 2.0e-10
Match length 81
% identity 38
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 10382
Contig ID 18657_1.R1040
5'-most EST uaw700665034.h1
Method BLASTX
NCBI GI g4468048
BLAST score 336
E value 2.0e-31
Match length 152
% identity 46
NCBI Description (X78703) catechol O-methyltransferase [Vanilla planifolia]

Seq. No. 10383
Contig ID 18659_1.R1040
5'-most EST LIB3049-006-Q1-E1-A6

Seq. No. 10384
Contig ID 18663_1.R1040
5'-most EST LIB3106-095-Q1-K1-F10

Seq. No. 10385
Contig ID 18669_1.R1040
5'-most EST uC-gmrominsoy031f01b1

Seq. No. 10386
Contig ID 18669_2.R1040
5'-most EST LIB3106-013-Q1-K1-E6

Seq. No. 10387

Contig ID 18670_1.R1040
 5'-most EST LIB3049-005-Q1-E1-G7
 Method BLASTX
 NCBI GI g1086147
 BLAST score 450
 E value 1.0e-44
 Match length 131
 % identity 61
 NCBI Description protein S2 - Phalaris coerulescens >gi_556833_emb_CAA57520_
 (X81992) S2 [Phalaris coerulescens]

Seq. No. 10388
 Contig ID 18670_2.R1040
 5'-most EST LIB3107-015-Q1-K1-E10

Seq. No. 10389
 Contig ID 18670_3.R1040
 5'-most EST vzy700751450.h1

Seq. No. 10390
 Contig ID 18678_1.R1040
 5'-most EST LIB3049-005-Q1-E1-H4
 Method BLASTX
 NCBI GI g2498329
 BLAST score 593
 E value 1.0e-61
 Match length 127
 % identity 91
 NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir_S65571
 pattern-formation protein GNOM - Arabidopsis thaliana
 >gi_1209633 (U36433) GNOM gene product [Arabidopsis
 thaliana] >gi_1335997 (U56140) similar to the Saccharomyces
 cerevisiae Sec7 protein, GenBank Accession Number J03918
 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the
 Saccharomyces cerevisiae Sec7 protein, GenBank Accession
 Number J03918 [Arabidopsis thaliana]

Seq. No. 10391
 Contig ID 18680_1.R1040
 5'-most EST LIB3094-043-Q1-K1-C9
 Method BLASTX
 NCBI GI g4544399
 BLAST score 745
 E value 3.0e-79
 Match length 177
 % identity 81
 NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
 thaliana]

Seq. No. 10392
 Contig ID 18683_1.R1040
 5'-most EST LIB3049-005-Q1-E1-H9

Seq. No. 10393
 Contig ID 18686_1.R1040
 5'-most EST LIB3049-005-Q1-E1-F10
 Method BLASTX

BLAST score 465
 E value 2.0e-46
 Match length 127
 % identity 72
 NCBI Description (U88061) SNF5 homolog BSH [Arabidopsis thaliana]

Seq. No. 10418
 Contig ID 18749_1.R1040
 5'-most EST LIB3170-021-Q1-K1-B5

Seq. No. 10419
 Contig ID 18750_1.R1040
 5'-most EST LIB3049-005-Q1-E1-B1
 Method BLASTX
 NCBI GI g3970680
 BLAST score 275
 E value 3.0e-24
 Match length 108
 % identity 52
 NCBI Description (AL034388) 67A9.b [Drosophila melanogaster]

Seq. No. 10420
 Contig ID 18750_2.R1040
 5'-most EST pmv700889336.h1
 Method BLASTX
 NCBI GI g3970680
 BLAST score 105
 E value 1.0e-11
 Match length 99
 % identity 46
 NCBI Description (AL034388) 67A9.b [Drosophila melanogaster]

Seq. No. 10421
 Contig ID 18750_3.R1040
 5'-most EST uC-gmronoir064h03b1

Seq. No. 10422
 Contig ID 18750_4.R1040
 5'-most EST jex700906670.h1

Seq. No. 10423
 Contig ID 18751_1.R1040
 5'-most EST sat701011064.h1
 Method BLASTX
 NCBI GI g3395938
 BLAST score 781
 E value 4.0e-83
 Match length 251
 % identity 50
 NCBI Description (AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No. 10424
 Contig ID 18753_1.R1040
 5'-most EST LIB3170-022-Q1-K1-B2
 Method BLASTX
 NCBI GI g3269287

Method	BLASTX
NCBI GI	g2500354
BLAST score	542
E value	2.0e-55
Match length	117
% identity	85
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]
Seq. No.	10444
Contig ID	18801_1.R1040
5'-most EST	g5677221
Seq. No.	10445
Contig ID	18801_2.R1040
5'-most EST	LIB3094-082-Q1-K1-D2
Method	BLASTX
NCBI GI	g4220534
BLAST score	494
E value	1.0e-49
Match length	199
% identity	51
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]
Seq. No.	10446
Contig ID	18814_1.R1040
5'-most EST	asn701137579.h1
Seq. No.	10447
Contig ID	18815_1.R1040
5'-most EST	leu701151423.h1
Seq. No.	10448
Contig ID	18816_1.R1040
5'-most EST	LIB3170-023-Q1-K1-B11
Seq. No.	10449
Contig ID	18817_1.R1040
5'-most EST	LIB3170-023-Q1-K1-B3
Seq. No.	10450
Contig ID	18820_1.R1040
5'-most EST	LIB3049-004-Q1-E1-C2
Method	BLASTX
NCBI GI	g2244800
BLAST score	326
E value	2.0e-30
Match length	106
% identity	61
NCBI Description	(Z97336) carnitine racemase homolog [Arabidopsis thaliana]
Seq. No.	10451
Contig ID	18821_1.R1040
5'-most EST	LIB3170-024-Q1-K1-B7
Seq. No.	10452
Contig ID	18823_1.R1040

5'-most EST LIB3170-024-Q1-K1-B8

Seq. No. 10453
 Contig ID 18830_1.R1040
 5'-most EST jC-gmf102220075b05d1
 Method BLASTX
 NCBI GI g3193296
 BLAST score 848
 E value 5.0e-91
 Match length 224
 % identity 67
 NCBI Description (AF069298) similar to pectinesterase [Arabidopsis thaliana]

Seq. No. 10454
 Contig ID 18831_1.R1040
 5'-most EST LIB3049-004-Q1-E1-A10
 Method BLASTX
 NCBI GI g3953479
 BLAST score 173
 E value 3.0e-12
 Match length 58
 % identity 57
 NCBI Description (AC002328) F2202.24 [Arabidopsis thaliana]

Seq. No. 10455
 Contig ID 18832_1.R1040
 5'-most EST LIB3170-023-Q1-K1-B10

Seq. No. 10456
 Contig ID 18834_1.R1040
 5'-most EST LIB3170-023-Q1-K1-B8

Seq. No. 10457
 Contig ID 18842_1.R1040
 5'-most EST LIB3049-003-Q1-E1-F9
 Method BLASTX
 NCBI GI g2462737
 BLAST score 309
 E value 2.0e-28
 Match length 126
 % identity 49
 NCBI Description (AC002292) similar to "Mx" GTP-binding proteins [Arabidopsis thaliana]

Seq. No. 10458
 Contig ID 18844_1.R1040
 5'-most EST gsv701047810.h1

Seq. No. 10459
 Contig ID 18844_2.R1040
 5'-most EST LIB3056-010-Q1-N1-E12

Seq. No. 10460
 Contig ID 18849_1.R1040
 5'-most EST uC-gmrominsoyl53d04b1
 Method BLASTX
 NCBI GI g3004549

BLAST score 358
 E value 2.0e-33
 Match length 177
 % identity 45
 NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]
 >gi_4185152 (AC005724) unknown protein [Arabidopsis thaliana]

Seq. No. 10461
 Contig ID 18849_2.R1040
 5'-most EST LIB3049-003-Q1-E1-G4
 Method BLASTX
 NCBI GI g3004549
 BLAST score 155
 E value 4.0e-13
 Match length 95
 % identity 48
 NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]
 >gi_4185152 (AC005724) unknown protein [Arabidopsis thaliana]

Seq. No. 10462
 Contig ID 18851_1.R1040
 5'-most EST LIB3049-003-Q1-E1-G6
 Method BLASTX
 NCBI GI g4105697
 BLAST score 984
 E value 1.0e-107
 Match length 233
 % identity 77
 NCBI Description (AF049870) thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 10463
 Contig ID 18851_3.R1040
 5'-most EST uC-gmrominsoyl06b10b1
 Method BLASTX
 NCBI GI g4105697
 BLAST score 369
 E value 3.0e-35
 Match length 86
 % identity 74
 NCBI Description (AF049870) thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 10464
 Contig ID 18852_1.R1040
 5'-most EST LIB3170-024-Q1-K1-A1
 Method BLASTX
 NCBI GI g3036840
 BLAST score 216
 E value 1.0e-17
 Match length 87
 % identity 48
 NCBI Description (AJ222967) cystinosin [Homo sapiens]
 >gi_3036851_emb_CAA75882_ (Y15924) cystinosin [Homo sapiens]

Seq. No. 10465

Contig ID 18865_1.R1040
 5'-most EST LIB3049-003-Q1-E1-E8
 Method BLASTX
 NCBI GI g3228517
 BLAST score 263
 E value 7.0e-23
 Match length 97
 % identity 63
 NCBI Description (AF007788) ETTIN [Arabidopsis thaliana]

Seq. No. 10466
 Contig ID 18867_1.R1040
 5'-most EST rca701002296.h1
 Method BLASTX
 NCBI GI g3080393
 BLAST score 963
 E value 1.0e-104
 Match length 290
 % identity 63
 NCBI Description (AL022603) NADH dehydrogenase like protein [Arabidopsis thaliana]

Seq. No. 10467
 Contig ID 18867_2.R1040
 5'-most EST LIB3138-050-Q1-N1-A6
 Method BLASTX
 NCBI GI g3080393
 BLAST score 289
 E value 5.0e-26
 Match length 86
 % identity 66
 NCBI Description (AL022603) NADH dehydrogenase like protein [Arabidopsis thaliana]

Seq. No. 10468
 Contig ID 18875_1.R1040
 5'-most EST uC-gmronoir070h12b1
 Method BLASTX
 NCBI GI g3927825
 BLAST score 1660
 E value 0.0e+00
 Match length 347
 % identity 91
 NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 10469
 Contig ID 18875_2.R1040
 5'-most EST LIB3139-050-P1-N1-F9
 Method BLASTX
 NCBI GI g2351580
 BLAST score 583
 E value 3.0e-60
 Match length 132
 % identity 85
 NCBI Description (U82433) thymidine diphospho-glucose 4-6-dehydratase homolog [Prunus armeniaca]

Seq. No. 10529
Contig ID 19048_1.R1040
5'-most EST kl1701208113.h1

Seq. No. 10530
Contig ID 19050_1.R1040
5'-most EST LIB3049-001-Q1-E1-C4
Method BLASTX
NCBI GI g3367537
BLAST score 148
E value 8.0e-10
Match length 70
% identity 49
NCBI Description (AC004392) Contains similarity to ANK repeat region of Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107 from *Caenorhabditis elegans* cosmid gb_U00049. This gene is continued from unannotated gene on BAC F19K23 gb_AC000375. [Arabid

Seq. No. 10531
Contig ID 19063_1.R1040
5'-most EST LIB3049-001-Q1-E1-D6

Seq. No. 10532
Contig ID 19065_1.R1040
5'-most EST g4306618
Method BLASTX
NCBI GI g1084391
BLAST score 432
E value 3.0e-42
Match length 124
% identity 63
NCBI Description endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG2) - common nasturtium (fragment) >gi_311837_emb_CAA48325_(X68255) cellulase [*Tropaeolum majus*]

Seq. No. 10533
Contig ID 19067_1.R1040
5'-most EST LIB3049-001-Q1-E1-A7

Seq. No. 10534
Contig ID 19069_1.R1040
5'-most EST LIB3170-020-Q1-K1-H6

Seq. No. 10535
Contig ID 19071_1.R1040
5'-most EST LIB3049-001-Q1-E1-B12

Seq. No. 10536
Contig ID 19093_1.R1040
5'-most EST LIB3050-022-Q1-K1-A7

Seq. No. 10537
Contig ID 19093_2.R1040
5'-most EST LIB3049-008-Q1-E1-A4

Seq. No. 10538

elongation factor Tu [*Arabidopsis thaliana*]

Seq. No. 10568
 Contig ID 19175_1.R1040
 5'-most EST LIB3049-047-Q1-E1-G8
 Method BLASTX
 NCBI GI g1076715
 BLAST score 278
 E value 2.0e-24
 Match length 92
 % identity 53
 NCBI Description abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [*Hordeum vulgare*]

Seq. No. 10569
 Contig ID 19180_1.R1040
 5'-most EST uC-gmrominsoyl86e08b1
 Method BLASTX
 NCBI GI g3142301
 BLAST score 295
 E value 2.0e-26
 Match length 101
 % identity 63
 NCBI Description (AC002411) Contains similarity to neural cell adhesion molecule 2, large isoform precursor gb_M76710 from *Xenopus laevis*, and beta transducin from *S. cerevisiae* gb_Q05946. ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101, gb_H3630

Seq. No. 10570
 Contig ID 19182_1.R1040
 5'-most EST LIB3049-051-Q1-E1-F5
 Method BLASTX
 NCBI GI g2262159
 BLAST score 961
 E value 1.0e-104
 Match length 265
 % identity 66
 NCBI Description (AC002329) predicted protein similar to *S.pombe* protein C5H10.03 [*Arabidopsis thaliana*]

Seq. No. 10571
 Contig ID 19185_1.R1040
 5'-most EST LIB3170-035-Q1-K1-A12
 Method BLASTX
 NCBI GI g4539351
 BLAST score 289
 E value 9.0e-26
 Match length 160
 % identity 39
 NCBI Description (AL035539) putative protein [*Arabidopsis thaliana*]

Seq. No. 10572
 Contig ID 19201_1.R1040
 5'-most EST LIB3106-100-Q1-K1-H11
 Method BLASTX
 NCBI GI g4105772

Method	BLASTX
NCBI GI	g4539348
BLAST score	934
E value	1.0e-101
Match length	247
% identity	68
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	10593
Contig ID	19240_2.R1040
5'-most EST	LIB3139-085-P1-N1-D11
Method	BLASTX
NCBI GI	g4539348
BLAST score	198
E value	8.0e-26
Match length	99
% identity	62
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

```
Seq. No.          10594
Contig ID         19240_3.R1040
5'-most EST      uC-gm̄rominsoy169c10b1
Method            BLASTX
NCBI GI           g4539348
BLAST score       347
E value           1.0e-32
Match length      86
% identity        69
NCBI Description  (AL035539) putative pollen allergen [Arabidopsis thaliana]
```

```
Seq. No.      10595
Contig ID     19242 1.R1040
5'-most EST   LIB3050-002-Q1-E1-D5
```

Seq. No.	10596
Contig ID	19242_2.R1040
5'-most EST	LIB3107-061-Q1-K1-F12

Seq. No.	10597
Contig ID	19246_1.R1040
5'-most EST	jC-qmst02400036g10d2

Seq. No.	10598
Contig ID	19247_1.R1040
5'-most EST	jC-gmfl02220061a10a1
Method	BLASTX
NCBI GI	g4006875
BLAST score	323
E value	8.0e-30
Match length	113
% identity	64
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	10599
Contig ID	19248_1.R1040
5'-most EST	dpv701102923.h1

Seq. No. 10600
 Contig ID 19248_2.R1040
 5'-most EST LIB3107-036-Q1-K1-D3
 Method BLASTX
 NCBI GI g2245060
 BLAST score 280
 E value 9.0e-25
 Match length 76
 % identity 64
 NCBI Description (Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No. 10601
 Contig ID 19250_1.R1040
 5'-most EST LIB3050-028-Q1-E1-C4

Seq. No. 10602
 Contig ID 19252_1.R1040
 5'-most EST wvk700685013.h1
 Method BLASTX
 NCBI GI g3281850
 BLAST score 788
 E value 3.0e-84
 Match length 175
 % identity 84
 NCBI Description (AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]

Seq. No. 10603
 Contig ID 19255_1.R1040
 5'-most EST uC-gmflminsoy080g12b1
 Method BLASTX
 NCBI GI g2213610
 BLAST score 245
 E value 3.0e-20
 Match length 150
 % identity 39
 NCBI Description (AC000103) F21J9.4 [Arabidopsis thaliana]

Seq. No. 10604
 Contig ID 19257_1.R1040
 5'-most EST LIB3050-027-Q1-E1-H4
 Method BLASTX
 NCBI GI g4314390
 BLAST score 396
 E value 4.0e-38
 Match length 142
 % identity 54
 NCBI Description (AC006232) putative calcium binding protein [Arabidopsis thaliana]

Seq. No. 10605
 Contig ID 19257_2.R1040
 5'-most EST zsg701124230.h1
 Method BLASTX
 NCBI GI g4314390
 BLAST score 337
 E value 2.0e-31

00000101 91048950

Contig ID 19264_1.R1040
5'-most EST dpv701102455.h1

Seq. No. 10614
Contig ID 19266_1.R1040
5'-most EST LIB3139-017-P1-N1-C1

Seq. No. 10615
Contig ID 19267_1.R1040
5'-most EST zhf700952901.h1
Method BLASTX
NCBI GI g2654868
BLAST score 306
E value 4.0e-52
Match length 174
% identity 66
NCBI Description (AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No. 10616
Contig ID 19268_1.R1040
5'-most EST jC-gmf102220097f01a1

Seq. No. 10617
Contig ID 19268_2.R1040
5'-most EST LIB3051-027-Q1-K1-G5

Seq. No. 10618
Contig ID 19274_1.R1040
5'-most EST LIB3050-027-Q1-E1-F3
Method BLASTN
NCBI GI g287563
BLAST score 77
E value 6.0e-35
Match length 327
% identity 91
NCBI Description Vigna radiata arg2 mRNA

Seq. No. 10619
Contig ID 19274_2.R1040
5'-most EST LIB3050-006-Q1-E1-G12
Method BLASTN
NCBI GI g287563
BLAST score 90
E value 1.0e-42
Match length 338
% identity 90
NCBI Description Vigna radiata arg2 mRNA

Seq. No. 10620
Contig ID 19275_1.R1040
5'-most EST LIB3139-084-P1-N1-H2

Seq. No. 10621
Contig ID 19275_2.R1040
5'-most EST asn701132347.h1

Seq. No. 10622

090100

Seq. No.	10624
Contig ID	19288_2.R1040
5'-most EST	jex700906632.h1

```
Seq. No.      10626
Contig ID     19293_2.R1040
5'-most EST   LIB3051-037-Q1-K1-A1
Method        BLASTX
NCBI GI       g4455351
BLAST score    298
E value        8.0e-27
Match length   82
% identity     66
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
```

```
Seq. No.          10627
Contig ID         19299_1.R1040
5'-most EST      leu701148775.h1
Method            BLASTX
NCBI GI           g1651451
BLAST score       517
E value           2.0e-52
Match length      137
% identity        70
NCBI Description  (D90730) Asparaginyl-tRNA synthetase (EC 6.1.1.22)
                  (asparagine-tRNA ligase) (asnRS). [Escherichia coli]
```

1852

Method BLASTX
 NCBI GI g3738332
 BLAST score 164
 E value 1.0e-11
 Match length 88
 % identity 51
 NCBI Description (AC005170) putative eukaryotic initiation factor
 [Arabidopsis thaliana]

Seq. No. 10662
 Contig ID 19359_1.R1040
 5'-most EST LIB3050-026-Q1-K1-H1
 Method BLASTX
 NCBI GI g3928862
 BLAST score 144
 E value 5.0e-09
 Match length 125
 % identity 30
 NCBI Description (AF089710) disease resistance protein RPP8 [Arabidopsis
 thaliana]

Seq. No. 10663
 Contig ID 19360_1.R1040
 5'-most EST LIB3051-115-Q1-K1-C4
 Method BLASTX
 NCBI GI g282963
 BLAST score 579
 E value 9.0e-60
 Match length 133
 % identity 81
 NCBI Description transforming protein (myb) homolog (clone myb.Ph2) - garden
 petunia >gi_20561_emb_CAA78387_ (Z13997) protein 2 [Petunia
 x hybrida]

Seq. No. 10664
 Contig ID 19362_1.R1040
 5'-most EST uxk700672889.h1

Seq. No. 10665
 Contig ID 19364_1.R1040
 5'-most EST uC-gmronoir043h01b1
 Method BLASTX
 NCBI GI g2829862
 BLAST score 773
 E value 1.0e-129
 Match length 443
 % identity 52
 NCBI Description (AC002396) Similar to glucosyltransferases [Arabidopsis
 thaliana]

Seq. No. 10666
 Contig ID 19367_1.R1040
 5'-most EST LIB3050-026-Q1-K1-E7

Seq. No. 10667
 Contig ID 19367_2.R1040
 5'-most EST sat701009408.h1

Seq. No. 10699
 Contig ID 19447_1.R1040
 5'-most EST fua701037771.h1
 Method BLASTX
 NCBI GI g477819
 BLAST score 1102
 E value 1.0e-121
 Match length 268
 % identity 78
 NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No. 10700
 Contig ID 19447_2.R1040
 5'-most EST LIB3170-046-Q1-J1-D12
 Method BLASTX
 NCBI GI g477280
 BLAST score 242
 E value 2.0e-20
 Match length 57
 % identity 75
 NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato >gi_410633_bbs_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa]

Seq. No. 10701
 Contig ID 19452_1.R1040
 5'-most EST LIB3050-025-Q1-K1-E10
 Method BLASTX
 NCBI GI g3402709
 BLAST score 659
 E value 3.0e-69
 Match length 179
 % identity 54
 NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 10702
 Contig ID 19453_1.R1040
 5'-most EST LIB3139-116-P1-N1-F11

Seq. No. 10703
 Contig ID 19455_1.R1040
 5'-most EST LIB3050-025-Q1-K1-E6

Seq. No. 10704
 Contig ID 19456_1.R1040
 5'-most EST jC-gmf102220056b02a1
 Method BLASTX
 NCBI GI g3928543
 BLAST score 1598
 E value 1.0e-178
 Match length 468

Seq. No. 10711
 Contig ID 19489_1.R1040
 5'-most EST g4293317
 Method BLASTX
 NCBI GI g1730081
 BLAST score 504
 E value 9.0e-51
 Match length 155
 % identity 67
 NCBI Description PROTEIN L1R18B (LLPR10.1B) >gi_1039336_emb_CAA56299
 (X79975) L1R18B [Lupinus luteus] >gi_2183277 (AF002278)
 LLPR10.1B [Lupinus luteus]

Seq. No. 10712
 Contig ID 19489_2.R1040
 5'-most EST yz1700966962.h1
 Method BLASTX
 NCBI GI g1703042
 BLAST score 367
 E value 1.0e-34
 Match length 157
 % identity 42
 NCBI Description ABA-RESPONSIVE PROTEIN ABR17 >gi_629631_pir_S42649
 abscisic acid-responsive protein ABR17 - garden pea
 >gi_20631_emb_CAA78829_ (Z15128) ABA-responsive protein
 [Pisum sativum]

Seq. No. 10713
 Contig ID 19489_3.R1040
 5'-most EST seb700650946.h1
 Method BLASTX
 NCBI GI g1730080
 BLAST score 163
 E value 2.0e-11
 Match length 58
 % identity 57
 NCBI Description PROTEIN L1R18A (LLPR10.1A) >gi_1039334_emb_CAA56298
 (X79974) L1R18A [Lupinus luteus] >gi_2183275 (AF002277)
 LLPR10.1A [Lupinus luteus]

Seq. No. 10714
 Contig ID 19490_1.R1040
 5'-most EST LIB3109-029-Q1-K1-F7

Seq. No. 10715
 Contig ID 19492_1.R1040
 5'-most EST jC-gmf102220126c10a1

Seq. No. 10716
 Contig ID 19492_2.R1040
 5'-most EST hrw701058618.h1

Seq. No. 10717
 Contig ID 19493_1.R1040
 5'-most EST LIB3050-025-Q1-K1-B6
 Method BLASTX

BLAST score 231
 E value 3.0e-19
 Match length 51
 % identity 86
 NCBI Description PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)
 >gi_1665831_dbj_BAA13640_(D88541) phosphoserine
 aminotransferase [Arabidopsis thaliana]
 >gi_2804260_dbj_BAA24441_(AB010408) phosphoserine
 aminotransferase [Arabidopsis thaliana]
 >gi_3367581_emb_CAA20033_(AL031135) phosphoserine
 aminotransferase [Arabidopsis thaliana]

Seq. No. 10723
 Contig ID 19515_2.R1040
 5'-most EST LIB3093-016-Q1-K1-C11
 Method BLASTN
 NCBI GI g2804259
 BLAST score 150
 E value 2.0e-78
 Match length 446
 % identity 83
 NCBI Description Arabidopsis thaliana DNA for phosphoserine
 aminotransferase, complete cds

Seq. No. 10724
 Contig ID 19515_3.R1040
 5'-most EST jsh701065269.h1
 Method BLASTN
 NCBI GI g2804259
 BLAST score 93
 E value 1.0e-44
 Match length 189
 % identity 88
 NCBI Description Arabidopsis thaliana DNA for phosphoserine
 aminotransferase, complete cds

Seq. No. 10725
 Contig ID 19516_1.R1040
 5'-most EST jC-gmf102220050c05a1

Seq. No. 10726
 Contig ID 19517_1.R1040
 5'-most EST LIB3050-024-Q1-K1-F11
 Method BLASTX
 NCBI GI g2832658
 BLAST score 244
 E value 2.0e-20
 Match length 94
 % identity 51
 NCBI Description (AL021710) putative protein [Arabidopsis thaliana]

Seq. No. 10727
 Contig ID 19517_2.R1040
 5'-most EST zzp700834035.h1
 Method BLASTX
 NCBI GI g2832658
 BLAST score 193

E value	4.0e-15
Match length	58
% identity	57
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]
Seq. No.	10728
Contig ID	19518_1.R1040
5'-most EST	LIB3050-024-Q1-K1-F12
Seq. No.	10729
Contig ID	19520_1.R1040
5'-most EST	LIB3050-024-Q1-K1-F4
Method	BLASTX
NCBI GI	g417148
BLAST score	379
E value	3.0e-39
Match length	138
% identity	61
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi_99912_pir_A33654 heat shock protein 26A - soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]
Seq. No.	10730
Contig ID	19521_1.R1040
5'-most EST	wrg700788594.h1
Method	BLASTX
NCBI GI	g4335715
BLAST score	586
E value	9.0e-71
Match length	291
% identity	51
NCBI Description	(AC006248) putative immediate-early salicylate-induced glucosyltransferase [Arabidopsis thaliana]
Seq. No.	10731
Contig ID	19528_1.R1040
5'-most EST	uC-gmropic010a04b1
Seq. No.	10732
Contig ID	19530_1.R1040
5'-most EST	pxt700945228.h1
Method	BLASTX
NCBI GI	g4510375
BLAST score	207
E value	3.0e-16
Match length	123
% identity	51
NCBI Description	(AC007017) putative homeotic protein BEL1 [Arabidopsis thaliana]
Seq. No.	10733
Contig ID	19533_1.R1040
5'-most EST	bth700843865.h1
Seq. No.	10734
Contig ID	19534_1.R1040
5'-most EST	LIB3050-024-Q1-K1-D6

BLAST score 999
 E value 1.0e-108
 Match length 387
 % identity 55
 NCBI Description serpin - barley >gi_19071_emb_CAA78822_ (Z15116) protein zx
 [Hordeum vulgare] >gi_444778_prf__1908213A protein Zx
 [Hordeum vulgare]

Seq. No. 10749
 Contig ID 19569_3.R1040
 5'-most EST wrg700787582.h1
 Method BLASTX
 NCBI GI g421989
 BLAST score 150
 E value 1.0e-09
 Match length 59
 % identity 51
 NCBI Description serpin - barley >gi_19071_emb_CAA78822_ (Z15116) protein zx
 [Hordeum vulgare] >gi_444778_prf__1908213A protein Zx
 [Hordeum vulgare]

Seq. No. 10750
 Contig ID 19582_1.R1040
 5'-most EST gbt700547938.h1
 Method BLASTX
 NCBI GI g4544409
 BLAST score 343
 E value 5.0e-32
 Match length 103
 % identity 59
 NCBI Description (AC006955) putative transcription factor [Arabidopsis
 thaliana]

Seq. No. 10751
 Contig ID 19582_2.R1040
 5'-most EST LIB3050-023-Q1-K1-G4
 Method BLASTX
 NCBI GI g4544409
 BLAST score 224
 E value 2.0e-18
 Match length 69
 % identity 58
 NCBI Description (AC006955) putative transcription factor [Arabidopsis
 thaliana]

Seq. No. 10752
 Contig ID 19584_1.R1040
 5'-most EST LIB3050-023-Q1-K1-G6
 Method BLASTX
 NCBI GI g4567203
 BLAST score 277
 E value 1.0e-24
 Match length 63
 % identity 84
 NCBI Description (AC007168) putative beta-hydroxyacyl-ACP dehydratase
 [Arabidopsis thaliana]

Contig ID	19625_4.R1040
5'-most EST	uC-gmrominsoy231b03b1
Method	BLASTX
NCBI GI	g4544409
BLAST score	259
E value	2.0e-22
Match length	88
% identity	53
NCBI Description	(AC006955) putative transcription factor [Arabidopsis thaliana]
Seq. No.	10776
Contig ID	19626_1.R1040
5'-most EST	ejt700606274.h1
Method	BLASTX
NCBI GI	g1730560
BLAST score	2686
E value	0.0e+00
Match length	557
% identity	91
NCBI Description	ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi_510932_emb_CAA84494_(Z35117) alpha 1,4-glucan phosphorylase type H [Vicia faba]
Seq. No.	10777
Contig ID	19627_1.R1040
5'-most EST	LIB3050-023-Q1-K1-E3
Seq. No.	10778
Contig ID	19633_1.R1040
5'-most EST	crh700851363.h1
Method	BLASTX
NCBI GI	g4455251
BLAST score	625
E value	8.0e-77
Match length	206
% identity	75
NCBI Description	(AL035523) magnesium-protoporphyrin IX methyltransferase-like protein [Arabidopsis thaliana]
Seq. No.	10779
Contig ID	19640_1.R1040
5'-most EST	LIB3050-023-Q1-K1-C7
Seq. No.	10780
Contig ID	19644_1.R1040
5'-most EST	taw700659052.h1
Method	BLASTX
NCBI GI	g4093157
BLAST score	734
E value	2.0e-77
Match length	274
% identity	62
NCBI Description	(AF087936) phytochrome-associated protein 2 [Arabidopsis thaliana]
Seq. No.	10781

SECRET

Seq. No. 10803

Seq. No. 10816
 Contig ID 19724_1.R1040
 5'-most EST fua701038254.h1
 Method BLASTX
 NCBI GI g2245060
 BLAST score 686
 E value 5.0e-72
 Match length 204
 % identity 61
 NCBI Description (Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No. 10817
 Contig ID 19728_1.R1040
 5'-most EST LIB3050-022-Q1-K1-D10
 Method BLASTX
 NCBI GI g3386620
 BLAST score 592
 E value 2.0e-61
 Match length 134
 % identity 46
 NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No. 10818
 Contig ID 19729_1.R1040
 5'-most EST uC-gmrominsoy048d04b1
 Method BLASTX
 NCBI GI g3335376
 BLAST score 1170
 E value 1.0e-131
 Match length 313
 % identity 75
 NCBI Description (AC003028) putative ammonium transporter [Arabidopsis thaliana]

Seq. No. 10819
 Contig ID 19729_2.R1040
 5'-most EST uC-gmropic115g04b1
 Method BLASTX
 NCBI GI g3335376
 BLAST score 271
 E value 8.0e-24
 Match length 58
 % identity 90
 NCBI Description (AC003028) putative ammonium transporter [Arabidopsis thaliana]

Seq. No. 10820
 Contig ID 19733_1.R1040
 5'-most EST LIB3050-022-Q1-K1-A5
 Method BLASTX
 NCBI GI g3643608
 BLAST score 372
 E value 9.0e-36
 Match length 129
 % identity 61
 NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No. 10821
 Contig ID 19737_1.R1040
 5'-most EST LIB3050-022-Q1-K1-A9
 Method BLASTX
 NCBI GI g3461846
 BLAST score 312
 E value 2.0e-28
 Match length 91
 % identity 33
 NCBI Description (AC005315) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No. 10822
 Contig ID 19739_1.R1040
 5'-most EST fde700875824.h1
 Method BLASTX
 NCBI GI g2829910
 BLAST score 793
 E value 9.0e-85
 Match length 166
 % identity 19
 NCBI Description (AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]

Seq. No. 10823
 Contig ID 19739_2.R1040
 5'-most EST rlr700896417.h1
 Method BLASTX
 NCBI GI g2829910
 BLAST score 757
 E value 1.0e-80
 Match length 191
 % identity 76
 NCBI Description (AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]

Seq. No. 10824
 Contig ID 19744_1.R1040
 5'-most EST LIB3050-022-Q1-K1-B4

Seq. No. 10825
 Contig ID 19746_1.R1040
 5'-most EST pcp700989286.h1

Seq. No. 10826
 Contig ID 19756_1.R1040
 5'-most EST uC-gmrominsoy183d12b1
 Method BLASTX
 NCBI GI g4510345
 BLAST score 460
 E value 2.0e-45
 Match length 160
 % identity 54
 NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 10827

NCBI Description ACTIN-LIKE PROTEIN 3 >gi_881635 (U29610) Arp3 [Acanthamoeba castellanii]

Seq. No. 10833
Contig ID 19767_2.R1040
5'-most EST jC-gmst02400023b08a1
Method BLASTX
NCBI GI g1168329
BLAST score 498
E value 3.0e-50
Match length 175
% identity 54

NCBI Description ACTIN-LIKE PROTEIN 3 (ACTIN-LIKE PROTEIN 66B) (ACTIN-2) >gi_558568_emb_CAA50674_ (X71789) actin related protein [Drosophila melanogaster] >gi_1096138_prf_2111232A actin-related protein [Drosophila melanogaster]

Seq. No. 10834
Contig ID 19768_1.R1040
5'-most EST LIB3107-053-Q1-K1-A5
Method BLASTX
NCBI GI g2760834
BLAST score 948
E value 1.0e-103
Match length 278
% identity 70

NCBI Description (AC003105) putative nitrate transporter [Arabidopsis thaliana]

Seq. No. 10835
Contig ID 19768_2.R1040
5'-most EST kl1701205306.h1
Method BLASTX
NCBI GI g3912921
BLAST score 148
E value 3.0e-09
Match length 59
% identity 46

NCBI Description (AF001308) G/T DNA mismatch repair enzyme [Arabidopsis thaliana]

Seq. No. 10836
Contig ID 19768_3.R1040
5'-most EST taw700657702.h1

Seq. No. 10837
Contig ID 19769_1.R1040
5'-most EST LIB3050-021-Q1-K1-C2
Method BLASTX
NCBI GI g4454567
BLAST score 235
E value 2.0e-19
Match length 123
% identity 45

NCBI Description (AF128407) lipase homolog [Arabidopsis thaliana]

Seq. No. 10838

09684016.1010000

Contig ID 19774_1.R1040
5'-most EST LIB3050-021-Q1-K1-C9
Method BLASTX
NCBI GI g2147328
BLAST score 202
E value 5.0e-16
Match length 90
% identity 52
NCBI Description dioscorin class B - Dioscorea cayenensis (fragment)

Seq. No. 10839
Contig ID 19775_1.R1040
5'-most EST LIB3109-045-Q1-K1-D6
Method BLASTX
NCBI GI g2160184
BLAST score 143
E value 7.0e-09
Match length 107
% identity 41
NCBI Description (AC000132) ESTs gb_H37208,gb_H36853 come from this gene.
[Arabidopsis thaliana]

Seq. No. 10840
Contig ID 19790_1.R1040
5'-most EST LIB3107-006-Q1-K1-B5
Method BLASTX
NCBI GI g2501448
BLAST score 450
E value 9.0e-45
Match length 93
% identity 92
NCBI Description UBIQUITIN-LIKE PROTEIN SMT3 >gi_1707372_emb_CAA67923_
(X99609) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 10841
Contig ID 19791_1.R1040
5'-most EST g5677872

Seq. No. 10842
Contig ID 19791_2.R1040
5'-most EST LIB3050-021-Q1-K1-E12

Seq. No. 10843
Contig ID 19794_1.R1040
5'-most EST LIB3139-040-P1-N1-A3
Method BLASTX
NCBI GI g4558591
BLAST score 588
E value 2.0e-60
Match length 178
% identity 63
NCBI Description (AC006555) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No. 10844
Contig ID 19794_2.R1040
5'-most EST sat701004908.h1

Method BLASTX
 NCBI GI g4455206
 BLAST score 1230
 E value 1.0e-136
 Match length 324
 % identity 72
 NCBI Description (AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No. 10845
 Contig ID 19794_3.R1040
 5'-most EST LIB3092-045-Q1-K1-A4
 Method BLASTX
 NCBI GI g4455206
 BLAST score 351
 E value 3.0e-33
 Match length 99
 % identity 64
 NCBI Description (AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No. 10846
 Contig ID 19794_4.R1040
 5'-most EST LIB3092-030-Q1-K1-D5
 Method BLASTX
 NCBI GI g4455206
 BLAST score 251
 E value 2.0e-21
 Match length 77
 % identity 61
 NCBI Description (AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No. 10847
 Contig ID 19794_5.R1040
 5'-most EST jC-gmro02910043a11d1
 Method BLASTX
 NCBI GI g4558591
 BLAST score 242
 E value 2.0e-20
 Match length 62
 % identity 71
 NCBI Description (AC006555) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No. 10848
 Contig ID 19794_6.R1040
 5'-most EST jC-gmro02800026b05d1

Seq. No. 10849
 Contig ID 19795_1.R1040
 5'-most EST LIB3050-020-Q1-K1-H4

Seq. No. 10850
 Contig ID 19797_1.R1040
 5'-most EST LIB3050-020-Q1-K1-H6

Seq. No. 10851
 Contig ID 19801_1.R1040
 5'-most EST hyd700727614.h1

Seq. No. 10852
 Contig ID 19803_1.R1040
 5'-most EST pmv700888283.h1

Seq. No. 10853
 Contig ID 19804_1.R1040
 5'-most EST g4283486
 Method BLASTX
 NCBI GI g2104816
 BLAST score 220
 E value 2.0e-17
 Match length 174
 % identity 28
 NCBI Description (Y13092) alpha-adaptin [*Drosophila melanogaster*]

Seq. No. 10854
 Contig ID 19807_1.R1040
 5'-most EST LIB3050-021-Q1-K1-A6
 Method BLASTX
 NCBI GI g2342682
 BLAST score 290
 E value 6.0e-26
 Match length 76
 % identity 72
 NCBI Description (AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb_X95577). [*Arabidopsis thaliana*]

Seq. No. 10855
 Contig ID 19820_1.R1040
 5'-most EST LIB3050-015-Q1-E1-D10
 Method BLASTX
 NCBI GI g1871577
 BLAST score 433
 E value 1.0e-42
 Match length 158
 % identity 53
 NCBI Description (Y11553) putative 21kD protein precursor [*Medicago sativa*]

Seq. No. 10856
 Contig ID 19824_1.R1040
 5'-most EST LIB3050-020-Q1-K1-F2
 Method BLASTX
 NCBI GI g4508069
 BLAST score 385
 E value 5.0e-37
 Match length 149
 % identity 48
 NCBI Description (AC005882) 12246 [*Arabidopsis thaliana*]

Seq. No. 10857
 Contig ID 19838_1.R1040
 5'-most EST uC-gmrominsoy244f07b1
 Method BLASTX

NCBI GI	g3785983
BLAST score	320
E value	3.0e-29
Match length	153
% identity	43
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	10858
Contig ID	19838_2.R1040
5'-most EST	LIB3073-017-Q1-K1-E3
Method	BLASTX
NCBI GI	g3785983
BLAST score	253
E value	1.0e-21
Match length	119
% identity	43
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.      10859
Contig ID     19838_3.R1040
5'-most EST  leu701149924.h1
```

```
Seq. No.          10860
Contig ID         19842 1.R1040
5'-most EST      LIB3092-062-Q1-K1-C5
Method           BLASTX
NCBI GI          g1931638
BLAST score       706
E value          2.0e-74
Match length      277
% identity        58
NCBI Description  (U95973) transcription factor RUSH-1alpha isolog
                  [Arabidopsis thaliana]
```

Seq. No.	10861
Contig ID	19844_1.R1040
5'-most EST	q4292527

```
Seq. No.      10862
Contig ID     19846_1.R1040
5'-most EST   LIB3050-020-Q1-K1-C6
```

Seq. No.	10863
Contig ID	19852_1.R1040
5'-most EST	LIB3051-107-Q1-K1-E10
Method	BLASTN
NCBI GI	g1209887
BLAST score	279
E value	1.0e-155
Match length	703
% identity	99
NCBI Description	Glycine max nonsymbiotic hemoglobin gene, complete cds

Seq. No.	10864
Contig ID	19852_2.R1040
5'-most EST	LIB3170-074-Q1-K1-E2
Method	BLASTN

Contig ID 20043 2.R1040
 5'-most EST LIB3139-097-P1-N1-A11
 Method BLASTX
 NCBI GI g3021268
 BLAST score 114
 E value 3.0e-11
 Match length 193
 % identity 36
 NCBI Description (AL022347) putative protein [Arabidopsis thaliana]

Seq. No. 10923
 Contig ID 20043 7.R1040
 5'-most EST eep700865965.h1

Seq. No. 10924
 Contig ID 20047 1.R1040
 5'-most EST g4313881

Seq. No. 10925
 Contig ID 20051 1.R1040
 5'-most EST trc700562631.h1
 Method BLASTX
 NCBI GI g1732247
 BLAST score 329
 E value 3.0e-37
 Match length 121
 % identity 64
 NCBI Description (U72762) transcription factor Myb1 [Nicotiana tabacum]

Seq. No. 10926
 Contig ID 20051 2.R1040
 5'-most EST trc700566792.h1
 Method BLASTX
 NCBI GI g1945279
 BLAST score 368
 E value 2.0e-35
 Match length 96
 % identity 64
 NCBI Description (Y11350) myb factor [Oryza sativa]

Seq. No. 10927
 Contig ID 20051 3.R1040
 5'-most EST uC-gmflminsoy043b11b1
 Method BLASTX
 NCBI GI g1946267
 BLAST score 247
 E value 2.0e-21
 Match length 61
 % identity 70
 NCBI Description (Y11415) myb [Oryza sativa]

Seq. No. 10928
 Contig ID 20056 1.R1040
 5'-most EST rlr700898958.h1
 Method BLASTX
 NCBI GI g1168940
 BLAST score 480

0000000000

```
Seq. No.          10939
Contig ID         20085_2.R1040
5'-most EST      zsg701127688.h1
Method            BLASTX
NCBI GI           g2832658
BLAST score       300
E value           1.0e-26
Match length      120
% identity        51
NCBI Description  (AL021710) putative protein [Arabidopsis thaliana]
```


BLAST score 248
 E value 8.0e-21
 Match length 144
 % identity 41
 NCBI Description (AC005990) F508.11 [Arabidopsis thaliana]

Seq. No. 10948
 Contig ID 20096_2.R1040
 5'-most EST uxk700670789.h1

Seq. No. 10949
 Contig ID 20097_1.R1040
 5'-most EST LIB3050-017-Q1-E1-B12

Seq. No. 10950
 Contig ID 20097_2.R1040
 5'-most EST bth700846843.h1

Seq. No. 10951
 Contig ID 20105_1.R1040
 5'-most EST LIB3050-016-Q1-E1-G9

Seq. No. 10952
 Contig ID 20106_1.R1040
 5'-most EST LIB3050-016-Q1-E1-G1

Seq. No. 10953
 Contig ID 20109_1.R1040
 5'-most EST pxt700943385.h1

Seq. No. 10954
 Contig ID 20115_1.R1040
 5'-most EST LIB3109-042-Q1-K1-A1

Method BLASTX
 NCBI GI g1351365
 BLAST score 153
 E value 5.0e-10
 Match length 48
 % identity 60
 NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 6.7 KD PROTEIN (CR6) >gi_2130002_pir_S68969 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) - potato >gi_633683_emb_CAA57768_(X82325) cytochrome c reductase subunit [Solanum tuberosum]

Seq. No. 10955
 Contig ID 20122_1.R1040
 5'-most EST g4289641
 Method BLASTX
 NCBI GI g2864615
 BLAST score 241
 E value 3.0e-20
 Match length 156
 % identity 33
 NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 10956
 Contig ID 20127_1.R1040

Method	BLASTX
NCBI GI	g3335335
BLAST score	472
E value	3.0e-47
Match length	121
% identity	73
NCBI Description	(AC004512) ESTs gb_F14113 and gb_T42122 come from this region. [Arabidopsis thaliana]
Seq. No.	10979
Contig ID	20215_1.R1040
5'-most EST	uC-gmrominsoy208b07b1
Method	BLASTX
NCBI GI	g121345
BLAST score	1683
E value	0.0e+00
Match length	341
% identity	91
NCBI Description	GLUTAMINE SYNTHETASE PR-2 (ISOZYME ALPHA) (GLUTAMATE--AMMONIA LIGASE) >gi_68593_pir_AJFBQA glutamate--ammonia ligase (EC 6.3.1.2) alpha, cytosolic - kidney bean >gi_21013_emb_CAA27632_(X04002) glutamine synthetase subunit (aa 1-356) [Phaseolus vulgaris] >gi_225068_prf_1208270B synthetase R2,Gln [Phaseolus vulgaris]
Seq. No.	10980
Contig ID	20215_2.R1040
5'-most EST	LIB3087-013-Q1-K1-C5
Method	BLASTN
NCBI GI	g21012
BLAST score	366
E value	0.0e+00
Match length	762
% identity	93
NCBI Description	Phaseolus vulgaris mRNA (pR-2) for glutamine synthetase (GS,EC 6.3.1.2)
Seq. No.	10981
Contig ID	20217_1.R1040
5'-most EST	LIB3050-015-Q1-E1-E12
Method	BLASTX
NCBI GI	g1491776
BLAST score	336
E value	1.0e-31
Match length	87
% identity	78
NCBI Description	(M37636) cationic peroxidase [Arachis hypogaea]
Seq. No.	10982
Contig ID	20228_1.R1040
5'-most EST	rca701001008.h1
Method	BLASTX
NCBI GI	g4567226
BLAST score	195
E value	1.0e-14
Match length	69

Contig ID 20281_2.R1040
5'-most EST seb700653544.h1

Seq. No. 10996
Contig ID 20288_1.R1040
5'-most EST LIB3170-055-Q1-K1-A3
Method BLASTX
NCBI GI g4469009
BLAST score 491
E value 3.0e-49
Match length 137
% identity 75
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 10997
Contig ID 20293_1.R1040
5'-most EST fde700871956.h1

Seq. No. 10998
Contig ID 20296_1.R1040
5'-most EST LIB3050-014-Q1-E1-F8
Method BLASTN
NCBI GI g1015315
BLAST score 66
E value 9.0e-29
Match length 82
% identity 95
NCBI Description Pisum sativum (clone PsRCI35-2) ribosomal protein L41 mRNA, complete cds

Seq. No. 10999
Contig ID 20297_1.R1040
5'-most EST LIB3050-014-Q1-E1-F9

Seq. No. 11000
Contig ID 20300_1.R1040
5'-most EST uC-gmropic030b10b1

Seq. No. 11001
Contig ID 20300_2.R1040
5'-most EST LIB3051-018-Q1-E1-H2

Seq. No. 11002
Contig ID 20305_1.R1040
5'-most EST uC-gmropic102d02b1
Method BLASTX
NCBI GI g4538939
BLAST score 1181
E value 1.0e-130
Match length 254
% identity 87
NCBI Description (AL049483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]

Seq. No. 11003
Contig ID 20308_1.R1040
5'-most EST LIB3050-014-Q1-E1-D12

Method BLASTX
 NCBI GI g2642215
 BLAST score 304
 E value 2.0e-27
 Match length 79
 % identity 70
 NCBI Description (AF030386) NOI protein [Arabidopsis thaliana]

Seq. No. 11004
 Contig ID 20312_1.R1040
 5'-most EST LIB3092-016-Q1-K1-G8

Seq. No. 11005
 Contig ID 20313_1.R1040
 5'-most EST LIB3050-003-Q1-E1-F3

Seq. No. 11006
 Contig ID 20313_2.R1040
 5'-most EST LIB3050-014-Q1-E1-D7

Seq. No. 11007
 Contig ID 20316_1.R1040
 5'-most EST LIB3050-014-Q1-E1-E11

Seq. No. 11008
 Contig ID 20317_1.R1040
 5'-most EST LIB3050-014-Q1-E1-C3
 Method BLASTX
 NCBI GI g3335376
 BLAST score 300
 E value 2.0e-27
 Match length 73
 % identity 73
 NCBI Description (AC003028) putative ammonium transporter [Arabidopsis thaliana]

Seq. No. 11009
 Contig ID 20319_1.R1040
 5'-most EST LIB3093-009-Q1-K1-E5
 Method BLASTX
 NCBI GI g3281848
 BLAST score 467
 E value 4.0e-46
 Match length 251
 % identity 49
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 11010
 Contig ID 20319_2.R1040
 5'-most EST LIB3050-014-Q1-E1-A6

Seq. No. 11011
 Contig ID 20319_3.R1040
 5'-most EST LIB3053-014-Q1-N1-H2
 Method BLASTX
 NCBI GI g4559352
 BLAST score 148

NCBI Description	(AC005623) putative bzip protein [Arabidopsis thaliana]
Seq. No.	11028
Contig ID	20360_1.R1040
5'-most EST	LIB3139-075-P1-N1-C2
Seq. No.	11029
Contig ID	20360_2.R1040
5'-most EST	zhf700963712.h1
Seq. No.	11030
Contig ID	20361_1.R1040
5'-most EST	jC-gmst02400069e10a1
Method	BLASTX
NCBI GI	g4454033
BLAST score	487
E value	6.0e-49
Match length	213
% identity	47
NCBI Description	(AL035394) putative potassium transport protein [Arabidopsis thaliana]
Seq. No.	11031
Contig ID	20362_1.R1040
5'-most EST	LIB3050-013-Q1-E1-F10
Seq. No.	11032
Contig ID	20365_1.R1040
5'-most EST	LIB3050-013-Q1-E1-F2
Seq. No.	11033
Contig ID	20368_1.R1040
5'-most EST	uC-gmrominsoy298f07b1
Seq. No.	11034
Contig ID	20370_1.R1040
5'-most EST	dpv701097078.h1
Seq. No.	11035
Contig ID	20371_1.R1040
5'-most EST	jC-gmle01810093c07d1
Method	BLASTX
NCBI GI	g3426048
BLAST score	239
E value	4.0e-20
Match length	63
% identity	78
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]
Seq. No.	11036
Contig ID	20373_1.R1040
5'-most EST	LIB3139-069-P1-N1-F4
Seq. No.	11037
Contig ID	20374_1.R1040
5'-most EST	LIB3138-029-Q1-N1-F7

5'-most EST	LIB3139-101-P1-N1-D5
Seq. No.	11051
Contig ID	20421_1.R1040
5'-most EST	LIB3051-020-Q1-E1-A11
Method	BLASTX
NCBI GI	g3738285
BLAST score	482
E value	4.0e-48
Match length	159
% identity	59
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	11052
Contig ID	20421_2.R1040
5'-most EST	g4314028
Method	BLASTX
NCBI GI	g3738285
BLAST score	313
E value	1.0e-28
Match length	102
% identity	57
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	11053
Contig ID	20421_3.R1040
5'-most EST	rlr700900790.h1
Method	BLASTX
NCBI GI	g3738285
BLAST score	181
E value	3.0e-13
Match length	57
% identity	61
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	11054
Contig ID	20421_4.R1040
5'-most EST	LIB3093-030-Q1-K1-H10
Method	BLASTX
NCBI GI	g3738285
BLAST score	173
E value	3.0e-12
Match length	87
% identity	43
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	11055
Contig ID	20427_1.R1040
5'-most EST	LIB3106-010-Q1-K1-D12
Seq. No.	11056
Contig ID	20431_1.R1040
5'-most EST	LIB3050-012-Q1-E1-F4
Seq. No.	11057
Contig ID	20433_1.R1040
5'-most EST	uC-gmrominsoy185f05b1

Seq. No. 11075
 Contig ID 20458_2.R1040
 5'-most EST LIB3051-031-Q1-K1-C2
 Method BLASTX
 NCBI GI g285741
 BLAST score 720
 E value 9.0e-76
 Match length 405
 % identity 42
 NCBI Description (D14550) EDGP precursor [Daucus carota]

Seq. No. 11076
 Contig ID 20458_3.R1040
 5'-most EST LIB3051-086-Q1-K1-B6

Seq. No. 11077
 Contig ID 20461_1.R1040
 5'-most EST LIB3050-012-Q1-E1-B6

Seq. No. 11078
 Contig ID 20464_1.R1040
 5'-most EST LIB3092-033-Q1-K1-A12
 Method BLASTX
 NCBI GI g4490736
 BLAST score 257
 E value 3.0e-22
 Match length 80
 % identity 34
 NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 11079
 Contig ID 20464_2.R1040
 5'-most EST gsv701048836.h1
 Method BLASTX
 NCBI GI g4490736
 BLAST score 416
 E value 9.0e-41
 Match length 166
 % identity 34
 NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 11080
 Contig ID 20466_1.R1040
 5'-most EST LIB3050-012-Q1-E1-C10

Seq. No. 11081
 Contig ID 20470_1.R1040
 5'-most EST fua701039064.h1
 Method BLASTX
 NCBI GI g4567228
 BLAST score 480
 E value 5.0e-48
 Match length 143
 % identity 65
 NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 11082
 Contig ID 20479 1.R1040
 5'-most EST LIB3050-011-Q1-E1-H9
 Method BLASTX
 NCBI GI g2832623
 BLAST score 703
 E value 5.0e-74
 Match length 207
 % identity 65
 NCBI Description (AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 11083
 Contig ID 20481 1.R1040
 5'-most EST gsv701056625.h1
 Method BLASTX
 NCBI GI g3953458
 BLAST score 948
 E value 1.0e-103
 Match length 215
 % identity 88
 NCBI Description (AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No. 11084
 Contig ID 20482 1.R1040
 5'-most EST kl1701213506.h1
 Method BLASTX
 NCBI GI g4539301
 BLAST score 822
 E value 8.0e-88
 Match length 355
 % identity 47
 NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No. 11085
 Contig ID 20487 1.R1040
 5'-most EST jsh701063973.h1

Seq. No. 11086
 Contig ID 20488 1.R1040
 5'-most EST LIB3107-014-Q1-K1-F2
 Method BLASTX
 NCBI GI g4049350
 BLAST score 538
 E value 1.0e-54
 Match length 220
 % identity 50
 NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 11087
 Contig ID 20497 1.R1040
 5'-most EST LIB3109-038-Q1-K1-G8

Seq. No. 11088
 Contig ID 20500 1.R1040
 5'-most EST LIB3139-047-P1-N1-B4

Method BLASTX
 NCBI GI g3309082
 BLAST score 656
 E value 1.0e-68
 Match length 164
 % identity 77
 NCBI Description (AF076251) calcineurin B-like protein 1 [Arabidopsis thaliana]

Seq. No. 11089
 Contig ID 20501_1.R1040
 5'-most EST dpv701102737.h1
 Method BLASTX
 NCBI GI g2598589
 BLAST score 853
 E value 1.0e-109
 Match length 275
 % identity 69
 NCBI Description (Y15367) MtN19 [Medicago truncatula]

Seq. No. 11090
 Contig ID 20501_2.R1040
 5'-most EST LIB3050-011-Q1-E1-D7
 Method BLASTX
 NCBI GI g2598589
 BLAST score 590
 E value 5.0e-61
 Match length 177
 % identity 64
 NCBI Description (Y15367) MtN19 [Medicago truncatula]

Seq. No. 11091
 Contig ID 20511_1.R1040
 5'-most EST LIB3050-011-Q1-E1-H4
 Method BLASTX
 NCBI GI g4406789
 BLAST score 433
 E value 9.0e-43
 Match length 114
 % identity 73
 NCBI Description (AC006532) putative glutamate decarboxylase [Arabidopsis thaliana]

Seq. No. 11092
 Contig ID 20513_1.R1040
 5'-most EST LIB3050-011-Q1-E1-G10

Seq. No. 11093
 Contig ID 20522_1.R1040
 5'-most EST LIB3107-049-Q1-K1-H5
 Method BLASTX
 NCBI GI g2244924
 BLAST score 335
 E value 2.0e-31
 Match length 87
 % identity 72
 NCBI Description (Z97339) glutaredoxin [Arabidopsis thaliana]

% identity	83
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]
Seq. No.	11156
Contig ID	20713_1.R1040
5'-most EST	jC-gmle01810006g11a1
Method	BLASTX
NCBI GI	g3482979
BLAST score	149
E value	6.0e-09
Match length	206
% identity	28
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana] >gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070) hypothetical protein [Arabidopsis thaliana]
Seq. No.	11157
Contig ID	20713_2.R1040
5'-most EST	LIB3170-062-Q1-J1-E3
Seq. No.	11158
Contig ID	20713_3.R1040
5'-most EST	epx701108675.h1
Seq. No.	11159
Contig ID	20715_1.R1040
5'-most EST	uC-gmropic091h07b1
Seq. No.	11160
Contig ID	20738_1.R1040
5'-most EST	pmv700894377.h1
Method	BLASTX
NCBI GI	g2289006
BLAST score	703
E value	6.0e-74
Match length	180
% identity	73
NCBI Description	(AC002335) glutathione peroxidase isolog [Arabidopsis thaliana]
Seq. No.	11161
Contig ID	20738_2.R1040
5'-most EST	pxt700946407.h1
Seq. No.	11162
Contig ID	20738_3.R1040
5'-most EST	LIB3170-049-Q1-K2-E6
Seq. No.	11163
Contig ID	20738_4.R1040
5'-most EST	jC-gmf102220108d04a1
Method	BLASTX
NCBI GI	g1946690
BLAST score	526
E value	1.0e-53
Match length	117

% identity 83
 NCBI Description (U94495) glutathione peroxidase [Arabidopsis thaliana]
 Seq. No. 11164
 Contig ID 20739_1.R1040
 5'-most EST LIB3050-008-Q1-E1-H4
 Method BLASTX
 NCBI GI g1699024
 BLAST score 727
 E value 9.0e-77
 Match length 233
 % identity 58
 NCBI Description (U78866) gene1000 [Arabidopsis thaliana] >gi_1699057
 (U78870) unknown [Arabidopsis thaliana]

Seq. No. 11165
 Contig ID 20739_2.R1040
 5'-most EST leu701146127.h1
 Method BLASTX
 NCBI GI g1699024
 BLAST score 350
 E value 4.0e-33
 Match length 100
 % identity 65
 NCBI Description (U78866) gene1000 [Arabidopsis thaliana] >gi_1699057
 (U78870) unknown [Arabidopsis thaliana]

Seq. No. 11166
 Contig ID 20739_3.R1040
 5'-most EST jC-gmst02400039a04a1
 Method BLASTX
 NCBI GI g1699024
 BLAST score 269
 E value 2.0e-23
 Match length 150
 % identity 43
 NCBI Description (U78866) gene1000 [Arabidopsis thaliana] >gi_1699057
 (U78870) unknown [Arabidopsis thaliana]

Seq. No. 11167
 Contig ID 20739_5.R1040
 5'-most EST eep700863855.h1

Seq. No. 11168
 Contig ID 20740_1.R1040
 5'-most EST trc700565610.h1
 Method BLASTX
 NCBI GI g1708424
 BLAST score 1036
 E value 1.0e-113
 Match length 262
 % identity 76
 NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590)
 isoflavone reductase-like protein [Lupinus albus]

Seq. No. 11169
 Contig ID 20741_1.R1040

0960387000

Seq. No.	11224
Contig ID	20947_2.R1040
5'-most EST	LIB3106-040-Q1-K1-D6

```
Seq. No.      11226
Contig ID     20950_2.R1040
5'-most EST   LIB3050-006-Q1-E1-B4
Method        BLASTN
NCBI GI       g2104680
BLAST score    65
E value       9.0e-28
Match length   214
% identity     87
NCBI Description V.faba mRNA for putative transcription factor (1556bp)
```

```
Seq. No.          11228
Contig ID         20952_1.R1040
5'-most EST      jC-gmst02400047e11a1
Method            BLASTX
NCBI GI           g627468
BLAST score       382
E value           2.0e-56
```


BLAST score 336
 E value 3.0e-31
 Match length 151
 % identity 49
 NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 11241
 Contig ID 20975_1.R1040
 5'-most EST LIB3087-012-Q1-K1-B10
 Method BLASTX
 NCBI GI g480618
 BLAST score 650
 E value 1.0e-67
 Match length 234
 % identity 61
 NCBI Description ATAF1 protein - Arabidopsis thaliana (fragment)
 >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis thaliana]

Seq. No. 11242
 Contig ID 20975_2.R1040
 5'-most EST pcp700989592.h1

Seq. No. 11243
 Contig ID 20996_1.R1040
 5'-most EST LIB3050-005-Q1-K1-G6

Seq. No. 11244
 Contig ID 20996_2.R1040
 5'-most EST LIB3094-040-Q1-K1-H1
 Method BLASTN
 NCBI GI g3510336
 BLAST score 73
 E value 9.0e-33
 Match length 77
 % identity 99
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
 K18J17, complete sequence [Arabidopsis thaliana]

Seq. No. 11245
 Contig ID 20996_3.R1040
 5'-most EST leu701148232.h1

Seq. No. 11246
 Contig ID 21005_1.R1040
 5'-most EST LIB3050-005-Q1-K1-B6
 Method BLASTX
 NCBI GI g1169017
 BLAST score 571
 E value 8.0e-59
 Match length 181
 % identity 27
 NCBI Description COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
 >gi_1078361_pir__B55123 coatomer complex beta' chain -
 yeast (Saccharomyces cerevisiae) >gi_595415 (U11237)
 betaprime COP [Saccharomyces cerevisiae]
 >gi_1246841_emb_CAA63359_ (X92670) see also U11237; yeast

000016-101000

Method	BLASTX
NCBI GI	g3582779
BLAST score	216
E value	8.0e-18
Match length	42
% identity	95
NCBI Description	(AF056282) peroxisomal targeting sequence 1 receptor [Nicotiana tabacum]
Seq. No.	11287
Contig ID	21167_1.R1040
5'-most EST	jC-gmst02400003d04d1
Seq. No.	11288
Contig ID	21169_1.R1040
5'-most EST	bth700846963.h1
Seq. No.	11289
Contig ID	21171_1.R1040
5'-most EST	jC-gmro02910068d03a1
Method	BLASTX
NCBI GI	g3395439
BLAST score	330
E value	2.0e-30
Match length	254
% identity	35
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]
Seq. No.	11290
Contig ID	21171_2.R1040
5'-most EST	fua701042933.h1
Seq. No.	11291
Contig ID	21171_3.R1040
5'-most EST	txt700736855.h1
Seq. No.	11292
Contig ID	21174_1.R1040
5'-most EST	LIB3094-006-Q1-K1-G10
Seq. No.	11293
Contig ID	21174_2.R1040
5'-most EST	jC-gmro02910005a07a1
Seq. No.	11294
Contig ID	21174_3.R1040
5'-most EST	leu701154556.h1
Seq. No.	11295
Contig ID	21175_1.R1040
5'-most EST	zpv700757458.h1
Method	BLASTX
NCBI GI	g2194120
BLAST score	155
E value	7.0e-10
Match length	116
% identity	39

E value	2.0e-96
Match length	401
% identity	49
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]
Seq. No.	11324
Contig ID	21263_1.R1040
5'-most EST	zhf700963542.h1
Method	BLASTX
NCBI GI	g2760086
BLAST score	425
E value	3.0e-52
Match length	178
% identity	19
NCBI Description	(Y16046) leucine-rich repeat protein [Arabidopsis thaliana]
Seq. No.	11325
Contig ID	21265_1.R1040
5'-most EST	LIB3053-008-Q1-N1-G11
Method	BLASTX
NCBI GI	g1480347
BLAST score	1788
E value	0.0e+00
Match length	378
% identity	87
NCBI Description	(X99419) ferredoxin NADP oxidoreductase [Pisum sativum]
Seq. No.	11326
Contig ID	21265_2.R1040
5'-most EST	asj700967432.h1
Method	BLASTN
NCBI GI	g1480346
BLAST score	57
E value	3.0e-23
Match length	129
% identity	86
NCBI Description	P.sativum mRNA for ferredoxin NADP oxidoreductase
Seq. No.	11327
Contig ID	21265_3.R1040
5'-most EST	jC-gmst02400064a05d1
Seq. No.	11328
Contig ID	21267_1.R1040
5'-most EST	crh700854281.h1
Seq. No.	11329
Contig ID	21269_1.R1040
5'-most EST	LIB3050-002-Q1-E1-D10
Seq. No.	11330
Contig ID	21270_1.R1040
5'-most EST	rlr700901075.h1
Method	BLASTX
NCBI GI	g1742951
BLAST score	902
E value	1.0e-97

Match length	201
% identity	83
NCBI Description	(Y09817) Ca2+-ATPase [Arabidopsis thaliana]
Seq. No.	11331
Contig ID	21272_1.R1040
5'-most EST	LIB3139-013-P1-N1-G6
Method	BLASTX
NCBI GI	g3219273
BLAST score	585
E value	3.0e-60
Match length	242
% identity	48
NCBI Description	(AB015316) MAP kinase kinase 5 [Arabidopsis thaliana]
Seq. No.	11332
Contig ID	21277_1.R1040
5'-most EST	LIB3050-002-Q1-E1-A6
Seq. No.	11333
Contig ID	21279_1.R1040
5'-most EST	LIB3050-002-Q1-E1-B1
Seq. No.	11334
Contig ID	21282_1.R1040
5'-most EST	LIB3050-002-Q1-E1-B2
Method	BLASTX
NCBI GI	g1730796
BLAST score	347
E value	9.0e-33
Match length	146
% identity	46
NCBI Description	HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC REGION >gi_2132760_pir_S60964 probable membrane protein YNL163c - yeast (Saccharomyces cerevisiae) >gi_1050790_emb_CAA63276_ (X92517) N1718 [Saccharomyces cerevisiae] >gi_1302132_emb_CAA96050_ (Z71439) ORF YNL163c [Saccharomyces cerevisiae]
Seq. No.	11335
Contig ID	21286_1.R1040
5'-most EST	LIB3170-067-Q1-K1-C8
Method	BLASTX
NCBI GI	g4008547
BLAST score	147
E value	4.0e-09
Match length	100
% identity	33
NCBI Description	(AL022072) arginine n-methyltransferase [Schizosaccharomyces pombe]
Seq. No.	11336
Contig ID	21288_1.R1040
5'-most EST	LIB3051-079-Q1-K1-D4
Seq. No.	11337
Contig ID	21296_1.R1040

09684016.101000

Seq. No.	11374
Contig ID	21373_1.R1040
5'-most EST	LIB3050-001-Q1-E1-H12
Method	BLASTX
NCBI GI	g2980806
BLAST score	588
E value	7.0e-61
Match length	176
% identity	48
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]
Seq. No.	11375
Contig ID	21375_1.R1040
5'-most EST	jC-gmf102220083a02a1
Method	BLASTX
NCBI GI	g3643598
BLAST score	325
E value	2.0e-29
Match length	89
% identity	62
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]
Seq. No.	11376
Contig ID	21376_1.R1040
5'-most EST	jC-gmro02800030a01d1
Seq. No.	11377
Contig ID	21383_1.R1040
5'-most EST	LIB3107-029-Q1-K1-F7
Method	BLASTX
NCBI GI	g2980767
BLAST score	533
E value	3.0e-54
Match length	170
% identity	63
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]
Seq. No.	11378
Contig ID	21386_1.R1040
5'-most EST	g4295843
Seq. No.	11379
Contig ID	21386_2.R1040
5'-most EST	g5606541
Method	BLASTX
NCBI GI	g1174199
BLAST score	216
E value	4.0e-17
Match length	130
% identity	45
NCBI Description	(U44760) S25-PR6 [Nicotiana tabacum]
Seq. No.	11380
Contig ID	21404_1.R1040
5'-most EST	zsg701118990.h1

5'-most EST bth700849155.h1
Method BLASTX
NCBI GI g2129575
BLAST score 557
E value 3.0e-57
Match length 142
% identity 77
NCBI Description DNA repair protein homolog XPBara - Arabidopsis thaliana

Seq. No. 11407
Contig ID 21457_1.R1040
5'-most EST wrg700789425.h2
Method BLASTX
NCBI GI g2914706
BLAST score 648
E value 7.0e-68
Match length 167
% identity 71
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No. 11408
Contig ID 21457_2.R1040
5'-most EST leu701147230.h1
Method BLASTX
NCBI GI g2914706
BLAST score 592
E value 3.0e-61
Match length 152
% identity 72
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No. 11409
Contig ID 21460_1.R1040
5'-most EST jC-gmf102220054g09a1
Method BLASTX
NCBI GI g1076660
BLAST score 1141
E value 1.0e-125
Match length 333
% identity 72
NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122
(S74753) MybSt1=Myb-related transcriptional activator
{DNA-binding domain repeats} [Solanum tuberosum=potatoes,
leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No. 11410
Contig ID 21460_3.R1040
5'-most EST ek1700968295.h1
Method BLASTX
NCBI GI g1076660
BLAST score 154
E value 2.0e-10
Match length 28
% identity 96
NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122
(S74753) MybSt1=Myb-related transcriptional activator
{DNA-binding domain repeats} [Solanum tuberosum=potatoes,

Match length 182
 % identity 31
 NCBI Description (U67953) contains similarity to C3HC4-class zinc finger
 (PS:PS00518) [Caenorhabditis elegans]

Seq. No. 11416
 Contig ID 21469_1.R1040
 5'-most EST LIB3051-026-Q1-K1-B7
 Method BLASTX
 NCBI GI g3152598
 BLAST score 389
 E value 1.0e-37
 Match length 113
 % identity 59
 NCBI Description (AC002986) Contains similarity to C2-HC type zinc finger
 protein C.e-MyT1 gb_U67079 from C. elegans and to
 hypersensitivity-related gene 201 isolog T28M21.14 from A.
 thaliana BAC gb_AF002109. [Arabidopsis thaliana]

Seq. No. 11417
 Contig ID 21472_1.R1040
 5'-most EST LIB3051-059-Q1-K2-E10
 Method BLASTX
 NCBI GI g2130078
 BLAST score 251
 E value 2.0e-21
 Match length 136
 % identity 46
 NCBI Description MADS-box protein 3 - rice >gi_886405 (L37528) MADS box
 protein [Oryza sativa]

Seq. No. 11418
 Contig ID 21472_2.R1040
 5'-most EST LIB3170-050-Q1-J1-C8

Seq. No. 11419
 Contig ID 21475_1.R1040
 5'-most EST jC-gmro02910060a03a1
 Method BLASTX
 NCBI GI g2865394
 BLAST score 185
 E value 2.0e-13
 Match length 118
 % identity 50
 NCBI Description (AF036949) basic leucine zipper protein [Zea mays]

Seq. No. 11420
 Contig ID 21476_1.R1040
 5'-most EST awf700836445.h1
 Method BLASTX
 NCBI GI g2062176
 BLAST score 859
 E value 4.0e-92
 Match length 356
 % identity 55
 NCBI Description (AC001645) Myb-related transcription activator (MybSt1)
 isolog [Arabidopsis thaliana]

BLAST score 393
 E value 5.0e-38
 Match length 169
 % identity 54
 NCBI Description (AJ223635) transcription factor IIA large subunit
 [Arabidopsis thaliana]

Seq. No. 11427
 Contig ID 21485_1.R1040
 5'-most EST awf700839210.h1
 Method BLASTX
 NCBI GI g3600059
 BLAST score 807
 E value 2.0e-86
 Match length 189
 % identity 76
 NCBI Description (AF080120) contains similarity to WB domains, G-beta
 repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03)
 [Arabidopsis thaliana]

Seq. No. 11428
 Contig ID 21488_1.R1040
 5'-most EST gsv701046512.h1
 Method BLASTX
 NCBI GI g4324495
 BLAST score 414
 E value 2.0e-40
 Match length 140
 % identity 68
 NCBI Description (AF105221) glutamyl-tRNA reductase precursor [Glycine max]

Seq. No. 11429
 Contig ID 21490_1.R1040
 5'-most EST dpv701099817.h1
 Method BLASTX
 NCBI GI g4510377
 BLAST score 309
 E value 3.0e-28
 Match length 140
 % identity 44
 NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No. 11430
 Contig ID 21491_1.R1040
 5'-most EST LIB3170-051-Q1-K1-B12
 Method BLASTX
 NCBI GI g4415931
 BLAST score 401
 E value 5.0e-39
 Match length 113
 % identity 65
 NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]
 >gi_4559393_gb_AAD23053.1 AC006526_18 (AC006526) unknown
 protein [Arabidopsis thaliana]

Seq. No. 11431
 Contig ID 21492_1.R1040

5'-most EST LIB3051-045-Q1-K1-D2
 Method BLASTX
 NCBI GI g4128208
 BLAST score 220
 E value 7.0e-18
 Match length 91
 % identity 52
 NCBI Description (AF076277) ethylene response factor 1 [Arabidopsis thaliana] >gi_4128210 (AF076278) ethylene response factor 1 [Arabidopsis thaliana]

Seq. No. 11432
 Contig ID 21494_1.R1040
 5'-most EST kl1701213301.h1
 Method BLASTX
 NCBI GI g2809251
 BLAST score 1185
 E value 1.0e-130
 Match length 351
 % identity 61
 NCBI Description (AC002560) F21B7.20 [Arabidopsis thaliana]

Seq. No. 11433
 Contig ID 21495_1.R1040
 5'-most EST jC-gmro02910040a03a1
 Method BLASTX
 NCBI GI g2462762
 BLAST score 762
 E value 5.0e-81
 Match length 248
 % identity 62
 NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 11434
 Contig ID 21496_1.R1040
 5'-most EST sat701012342.h1
 Method BLASTX
 NCBI GI g3193297
 BLAST score 761
 E value 5.0e-81
 Match length 184
 % identity 71
 NCBI Description (AF069298) similar to epoxide hydrolases [Arabidopsis thaliana]

Seq. No. 11435
 Contig ID 21497_1.R1040
 5'-most EST uC-gmrominsoy057h04b1

Seq. No. 11436
 Contig ID 21499_1.R1040
 5'-most EST LIB3051-082-Q1-K1-G3

Seq. No. 11437
 Contig ID 21500_1.R1040
 5'-most EST seb700652885.h1

Method	BLASTX
NCBI GI	g2827699
BLAST score	167
E value	1.0e-11
Match length	57
% identity	53
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.	11438
Contig ID	21500_2.R1040
5'-most EST	kl1701212039.h1
Method	BLASTX
NCBI GI	g2827699
BLAST score	167
E value	8.0e-12
Match length	57
% identity	51
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.	11439
Contig ID	21501_1.R1040
5'-most EST	fc-gmse700752437a2
Method	BLASTX
NCBI GI	g3309084
BLAST score	469
E value	8.0e-47
Match length	114
% identity	82
NCBI Description	(AF076252) calcineurin B-like protein 2 [Arabidopsis thaliana]
Seq. No.	11440
Contig ID	21501_3.R1040
5'-most EST	pcp700994873.h1
Method	BLASTX
NCBI GI	g3309084
BLAST score	195
E value	5.0e-15
Match length	55
% identity	67
NCBI Description	(AF076252) calcineurin B-like protein 2 [Arabidopsis thaliana]
Seq. No.	11441
Contig ID	21502_1.R1040
5'-most EST	uC-gmropic090g04b1
Method	BLASTX
NCBI GI	g3287270
BLAST score	1044
E value	1.0e-114
Match length	274
% identity	73
NCBI Description	(Y09533) involved in starch metabolism [Solanum tuberosum]
Seq. No.	11442
Contig ID	21504_1.R1040
5'-most EST	ncj700975676.h1

Method BLASTX
 NCBI GI g3738306
 BLAST score 160
 E value 2.0e-10
 Match length 76
 % identity 42
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 11443
 Contig ID 21505_1.R1040
 5'-most EST LIB3051-105-Q1-K1-G3

Seq. No. 11444
 Contig ID 21505_2.R1040
 5'-most EST taw700660105.h1

Seq. No. 11445
 Contig ID 21507_1.R1040
 5'-most EST LIB3051-020-Q1-E1-B12
 Method BLASTX
 NCBI GI g2465925
 BLAST score 254
 E value 8.0e-22
 Match length 116
 % identity 48
 NCBI Description (AF024649) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 11446
 Contig ID 21508_1.R1040
 5'-most EST LIB3051-107-Q1-K1-G11
 Method BLASTX
 NCBI GI g3298536
 BLAST score 505
 E value 3.0e-51
 Match length 139
 % identity 68
 NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]

Seq. No. 11447
 Contig ID 21509_1.R1040
 5'-most EST LIB3051-070-Q1-K1-F1
 Method BLASTN
 NCBI GI g3241925
 BLAST score 40
 E value 4.0e-13
 Match length 168
 % identity 89
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No. 11448
 Contig ID 21510_1.R1040
 5'-most EST pxt700943472.h1
 Method BLASTN
 NCBI GI g2264312
 BLAST score 37

Method BLASTX
 NCBI GI g2088651
 BLAST score 295
 E value 3.0e-26
 Match length 158
 % identity 42
 NCBI Description (AF002109) hypersensitivity-related gene 201 isolog
 [Arabidopsis thaliana]

Seq. No. 11455
 Contig ID 21518_1.R1040
 5'-most EST LIB3170-041-Q1-J1-F10
 Method BLASTX
 NCBI GI g4218141
 BLAST score 240
 E value 2.0e-19
 Match length 331
 % identity 30
 NCBI Description (AJ236702) HMR1 protein [Antirrhinum majus]

Seq. No. 11456
 Contig ID 21518_2.R1040
 5'-most EST kl1701204524.h2
 Method BLASTX
 NCBI GI g555655
 BLAST score 273
 E value 1.0e-23
 Match length 159
 % identity 55
 NCBI Description (U06712) DNA-binding protein [Nicotiana tabacum]

Seq. No. 11457
 Contig ID 21518_3.R1040
 5'-most EST jC-gmf102220051a02d1

Seq. No. 11458
 Contig ID 21518_4.R1040
 5'-most EST ssr700556645.h1

Seq. No. 11459
 Contig ID 21520_1.R1040
 5'-most EST asn701135640.h1
 Method BLASTX
 NCBI GI g4512667
 BLAST score 939
 E value 1.0e-107
 Match length 311
 % identity 64
 NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 11460
 Contig ID 21520_2.R1040
 5'-most EST ckk700605794.h2
 Method BLASTX
 NCBI GI g4512667
 BLAST score 171
 E value 5.0e-12

Match length 97
 % identity 56
 NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 11461
 Contig ID 21521_1.R1040
 5'-most EST LIB3170-057-Q1-K1-E2
 Method BLASTX
 NCBI GI g3107903
 BLAST score 186
 E value 1.0e-13
 Match length 61
 % identity 59
 NCBI Description (D83719) polycomb-like protein [Daucus carota]

Seq. No. 11462
 Contig ID 21522_1.R1040
 5'-most EST LIB3109-001-Q1-K2-A11
 Method BLASTX
 NCBI GI g3201618
 BLAST score 798
 E value 2.0e-85
 Match length 166
 % identity 85
 NCBI Description (AC004669) Sop2p-like protein [Arabidopsis thaliana]

Seq. No. 11463
 Contig ID 21522_2.R1040
 5'-most EST wvk700686490.h1
 Method BLASTX
 NCBI GI g3201618
 BLAST score 252
 E value 1.0e-21
 Match length 118
 % identity 58
 NCBI Description (AC004669) Sop2p-like protein [Arabidopsis thaliana]

Seq. No. 11464
 Contig ID 21523_1.R1040
 5'-most EST LIB3051-027-Q1-K1-A6
 Method BLASTX
 NCBI GI g1850546
 BLAST score 562
 E value 9.0e-58
 Match length 141
 % identity 80
 NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]

Seq. No. 11465
 Contig ID 21524_1.R1040
 5'-most EST uC-gmflminsoy018e09b1
 Method BLASTX
 NCBI GI g4539418
 BLAST score 477
 E value 7.0e-48
 Match length 153

% identity 59
NCBI Description (AL049171) caffeoyl-CoA O-methyltransferase-like protein [Arabidopsis thaliana]

Seq. No. 11466
Contig ID 21525 1.R1040
5'-most EST LIB3051-026-Q1-K1-G11
Method BLASTX
NCBI GI g4006848
BLAST score 665
E value 6.0e-70
Match length 168
% identity 79

NCBI Description (AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No. 11467
Contig ID 21526 2.R1040
5'-most EST rca700999839.h1
Method BLASTX
NCBI GI g3319342
BLAST score 537
E value 2.0e-54
Match length 252
% identity 45

NCBI Description (AF077407) similar to mitochondrial carrier proteins (Pfam: mit carr.hmm, score: 79.74 and 42.50) [Arabidopsis thaliana]

Seq. No. 11468
Contig ID 21528 1.R1040
5'-most EST jC-gm1e01810035d07a2
Method BLASTN
NCBI GI g1370155
BLAST score 120
E value 8.0e-61
Match length 204
% identity 90

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB11H

Seq. No. 11469
Contig ID 21528 2.R1040
5'-most EST LIB3051-114-Q1-K1-F1
Method BLASTN
NCBI GI g1370155
BLAST score 201
E value 1.0e-109
Match length 333
% identity 90

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB11H

Seq. No. 11470
Contig ID 21529 1.R1040
5'-most EST LIB3093-042-Q1-K1-A10
Method BLASTX
NCBI GI g3395938
BLAST score 623

BLAST score 1300
 E value 1.0e-144
 Match length 441
 % identity 36
 NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No. 11476
 Contig ID 21536_1.R1040
 5'-most EST LIB3109-043-Q1-K1-F1

Seq. No. 11477
 Contig ID 21537_1.R1040
 5'-most EST LIB3051-108-Q1-K1-A10
 Method BLASTX
 NCBI GI g2498565
 BLAST score 245
 E value 8.0e-21
 Match length 111
 % identity 41
 NCBI Description C-MYC BINDING PROTEIN MM-1 >gi_1731809_dbj_BAA14006_
 (D89667) c-myc binding protein [Homo sapiens]
 >gi_4505743_ref_NP_002615.1_pPFDN5_prefoldin

Seq. No. 11478
 Contig ID 21537_2.R1040
 5'-most EST pcp700993248.h1
 Method BLASTX
 NCBI GI g2498565
 BLAST score 232
 E value 3.0e-19
 Match length 111
 % identity 39
 NCBI Description C-MYC BINDING PROTEIN MM-1 >gi_1731809_dbj_BAA14006_
 (D89667) c-myc binding protein [Homo sapiens]
 >gi_4505743_ref_NP_002615.1_pPFDN5_prefoldin

Seq. No. 11479
 Contig ID 21538_1.R1040
 5'-most EST LIB3051-110-Q1-K1-G7
 Method BLASTX
 NCBI GI g4063751
 BLAST score 395
 E value 4.0e-38
 Match length 204
 % identity 43
 NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]
 >gi_4510409_gb_AAD21495.1_ (AC006929) putative white
 protein [Arabidopsis thaliana]

Seq. No. 11480
 Contig ID 21539_1.R1040
 5'-most EST asn701138037.h1
 Method BLASTX
 NCBI GI g3894387
 BLAST score 292
 E value 8.0e-26
 Match length 197

BLAST score 751
 E value 1.0e-79
 Match length 297
 % identity 54
 NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No. 11486
 Contig ID 21544 2.R1040
 5'-most EST uC-gmflminsoy011c06b1
 Method BLASTX
 NCBI GI g4539301
 BLAST score 121
 E value 4.0e-11
 Match length 97
 % identity 48
 NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No. 11487
 Contig ID 21545 1.R1040
 5'-most EST uC-gmflminsoy008g01b1
 Method BLASTX
 NCBI GI g2723391
 BLAST score 240
 E value 8.0e-20
 Match length 197
 % identity 36
 NCBI Description (AB007042) EXTR1 [Homo sapiens] >gi_2897905 (AF001690) EXT like protein 3 [Homo sapiens] >gi_3043562 dbj_BAA25445 (AB011091) KIAA0519 protein [Homo sapiens] >gi_4103884 (AF029231) EXT homolog [Homo sapiens] >gi_4503617_ref_NP_001431.1_pEXTL3_exostoses (multiple)-like

Seq. No. 11488
 Contig ID 21546 1.R1040
 5'-most EST LIB3170-059-Q1-K1-E5
 Method BLASTX
 NCBI GI g2213594
 BLAST score 868
 E value 2.0e-93
 Match length 257
 % identity 64
 NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 11489
 Contig ID 21572 1.R1040
 5'-most EST LIB3093-052-Q1-K1-D2
 Method BLASTX
 NCBI GI g1354466
 BLAST score 419
 E value 6.0e-41
 Match length 143
 % identity 59
 NCBI Description (U52910) U1 snRNP 70K truncated protein [Arabidopsis thaliana] >gi_1354468 (U52909) U1 snRNP 70K truncated

% identity	46
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]
Seq. No.	11495
Contig ID	21577_1.R1040
5'-most EST	g4396502
Method	BLASTX
NCBI GI	g320556
BLAST score	507
E value	7.0e-51
Match length	252
% identity	40
NCBI Description	chitinase (EC 3.2.1.14) precursor, basic - Arabidopsis thaliana >gi_166666 (M38240) basic chitinase [Arabidopsis thaliana]
Seq. No.	11496
Contig ID	21577_2.R1040
5'-most EST	leu701148149.h1
Method	BLASTX
NCBI GI	g2980793
BLAST score	421
E value	6.0e-41
Match length	164
% identity	47
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]
Seq. No.	11497
Contig ID	21578_1.R1040
5'-most EST	k11701202926.h1
Method	BLASTX
NCBI GI	g4406784
BLAST score	203
E value	6.0e-16
Match length	95
% identity	48
NCBI Description	(AC006532) putative oligopeptide transport protein [Arabidopsis thaliana]
Seq. No.	11498
Contig ID	21581_1.R1040
5'-most EST	seb700654218.h1
Method	BLASTX
NCBI GI	g2829912
BLAST score	486
E value	1.0e-64
Match length	158
% identity	84
NCBI Description	(AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]
Seq. No.	11499
Contig ID	21582_1.R1040
5'-most EST	LIB3093-057-Q1-K1-F9
Method	BLASTX
NCBI GI	g3297816
BLAST score	979

E value 1.0e-106
Match length 306
% identity 69
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 11500
Contig ID 21582_3.R1040
5'-most EST uC-gmronoir006h07b1
Method BLASTX
NCBI GI g3297816
BLAST score 508
E value 2.0e-51
Match length 149
% identity 64
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 11501
Contig ID 21586_1.R1040
5'-most EST jC-gmle01810012e02a1
Method BLASTX
NCBI GI g1549249
BLAST score 315
E value 5.0e-30
Match length 176
% identity 43
NCBI Description (U66620) SWI/SNF complex 60 KDa subunit [Mus musculus]

Seq. No. 11502
Contig ID 21587_1.R1040
5'-most EST ek1700968247.h1
Method BLASTX
NCBI GI g1431629
BLAST score 1396
E value 1.0e-155
Match length 398
% identity 63
NCBI Description (X99348) pectinacetylerase precursor [Vigna radiata]

Seq. No. 11503
Contig ID 21587_2.R1040
5'-most EST kl1701211669.h1
Method BLASTN
NCBI GI g1431628
BLAST score 35
E value 3.0e-10
Match length 43
% identity 95
NCBI Description V.radiata mRNA for pectinacetylerase

Seq. No. 11504
Contig ID 21589_1.R1040
5'-most EST LIB3093-023-Q1-K1-F8
Method BLASTX
NCBI GI g2160144
BLAST score 267
E value 5.0e-23
Match length 169

NCBI GI g2072393
 BLAST score 830
 E value 3.0e-89
 Match length 174
 % identity 92
 NCBI Description (U29168) similar to human Xeroderma pigmentosum group B DNA repair protein, Swiss-Prot Accession Number P19447 [Arabidopsis thaliana]

Seq. No. 11520
 Contig ID 21628_1.R1040
 5'-most EST ncj700988180.h1
 Method BLASTX
 NCBI GI g3201635
 BLAST score 413
 E value 2.0e-40
 Match length 132
 % identity 59
 NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No. 11521
 Contig ID 21629_1.R1040
 5'-most EST LIB3051-011-Q1-E1-H5
 Method BLASTX
 NCBI GI g3540181
 BLAST score 497
 E value 2.0e-50
 Match length 135
 % identity 74
 NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 11522
 Contig ID 21635_1.R1040
 5'-most EST LIB3051-002-Q1-E1-E10
 Method BLASTX
 NCBI GI g728906
 BLAST score 266
 E value 3.0e-23
 Match length 90
 % identity 56
 NCBI Description PROBABLE CALCIUM-TRANSPORTING ATPASE 5
 >gi_1077722_pir__S50669 hypothetical protein YER166w - yeast (Saccharomyces cerevisiae) >gi_603407 (U18922) Yer166wp [Saccharomyces cerevisiae]

Seq. No. 11523
 Contig ID 21637_1.R1040
 5'-most EST LIB3051-034-Q1-K1-E2
 Method BLASTX
 NCBI GI g1532171
 BLAST score 496
 E value 3.0e-50
 Match length 132
 % identity 70
 NCBI Description (U63815) AT.I.24-9 gene product [Arabidopsis thaliana]

Seq. No. 11524

5'-most EST bth700846162.h1
 Method BLASTX
 NCBI GI g2576361
 BLAST score 517
 E value 2.0e-52
 Match length 144
 % identity 66
 NCBI Description (U39782) lysine and histidine specific transporter
 [Arabidopsis thaliana]

Seq. No. 11530
 Contig ID 21645_1.R1040
 5'-most EST eep700868213.h1
 Method BLASTX
 NCBI GI g4008006
 BLAST score 501
 E value 1.0e-50
 Match length 152
 % identity 64
 NCBI Description (AF084034) receptor-like protein kinase [Arabidopsis
 thaliana]

Seq. No. 11531
 Contig ID 21646_1.R1040
 5'-most EST seb700650524.h1
 Method BLASTX
 NCBI GI g115473
 BLAST score 947
 E value 1.0e-102
 Match length 253
 % identity 71
 NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
 DEHYDRATASE) >gi_170219 (M94135) chloroplast carbonic
 anhydrase [Nicotiana tabacum] >gi_445610_prf__1909357A
 carbonic anhydrase [Nicotiana tabacum]

Seq. No. 11532
 Contig ID 21646_2.R1040
 5'-most EST uC-gmrominsoy247g12b1
 Method BLASTX
 NCBI GI g1168740
 BLAST score 581
 E value 5.0e-60
 Match length 140
 % identity 77
 NCBI Description CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi_882244
 (U19740) carbonic anhydrase 2 [Flaveria linearis]

Seq. No. 11533
 Contig ID 21646_3.R1040
 5'-most EST jsh701065528.h1
 Method BLASTX
 NCBI GI g1168740
 BLAST score 310
 E value 6.0e-35
 Match length 131
 % identity 60

Method BLASTX
 NCBI GI g4406780
 BLAST score 509
 E value 2.0e-51
 Match length 128
 % identity 75
 NCBI Description (AC006532) putative multispanning membrane protein
 [Arabidopsis thaliana]

Seq. No. 11539
 Contig ID 21655_1.R1040
 5'-most EST LIB3051-035-Q1-K1-C4
 Method BLASTX
 NCBI GI g2739386
 BLAST score 475
 E value 1.0e-47
 Match length 168
 % identity 59
 NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 11540
 Contig ID 21656_1.R1040
 5'-most EST LIB3051-037-Q1-K1-C4
 Method BLASTX
 NCBI GI g2224901
 BLAST score 263
 E value 7.0e-23
 Match length 136
 % identity 49
 NCBI Description (U67134) PcMYB1 protein [Petroselinum crispum]

Seq. No. 11541
 Contig ID 21656_2.R1040
 5'-most EST LIB3087-004-Q1-K1-G4
 Method BLASTX
 NCBI GI g2224899
 BLAST score 377
 E value 5.0e-36
 Match length 203
 % identity 47
 NCBI Description (U67133) DNA-binding protein PcMYB1 [Petroselinum crispum]

Seq. No. 11542
 Contig ID 21657_1.R1040
 5'-most EST dpv701103216.h1
 Method BLASTX
 NCBI GI g1786134
 BLAST score 207
 E value 1.0e-16
 Match length 97
 % identity 51
 NCBI Description (AB000451) PETHy;ZPT2-5 [Petunia x hybrida]

Seq. No. 11543
 Contig ID 21658_1.R1040
 5'-most EST zsg701129482.h1
 Method BLASTX

NCBI GI g4519417
 BLAST score 382
 E value 2.0e-36
 Match length 109
 % identity 62
 NCBI Description (AB024327) WD-40 repeat protein [Homo sapiens]

Seq. No. 11544
 Contig ID 21661_1.R1040
 5'-most EST fua701041663.h1
 Method BLASTX
 NCBI GI g3935138
 BLAST score 969
 E value 1.0e-105
 Match length 358
 % identity 54
 NCBI Description (AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No. 11545
 Contig ID 21662_1.R1040
 5'-most EST LIB3051-039-Q1-K1-B10
 Method BLASTX
 NCBI GI g2642450
 BLAST score 669
 E value 2.0e-70
 Match length 168
 % identity 77
 NCBI Description (AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi_3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No. 11546
 Contig ID 21665_1.R1040
 5'-most EST jC-gmst02400031f11a1
 Method BLASTX
 NCBI GI g4521322
 BLAST score 402
 E value 8.0e-39
 Match length 156
 % identity 53
 NCBI Description (U11790) mitotic centromere-associated kinesin [Cricetulus griseus]

Seq. No. 11547
 Contig ID 21665_3.R1040
 5'-most EST LIB3170-049-Q1-K2-E3
 Method BLASTX
 NCBI GI g2497528
 BLAST score 467
 E value 1.0e-46
 Match length 199
 % identity 50
 NCBI Description KINESIN-LIKE PROTEIN KIF2 (KINESIN-RELATED PROTEIN XKIF2) >gi_1171151 (U36486) kinesin-related protein XKIF2 [Xenopus laevis]

Seq. No. 11548

Contig ID 21665 4.R1040
 5'-most EST uC-gmflminsoy016g07b1
 Method BLASTN
 NCBI GI g4159706
 BLAST score 43
 E value 5.0e-15
 Match length 207
 % identity 80
 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence [Arabidopsis thaliana]

Seq. No. 11549
 Contig ID 21666 1.R1040
 5'-most EST hyd700728575.h1
 Method BLASTX
 NCBI GI g2864624
 BLAST score 558
 E value 1.0e-90
 Match length 437
 % identity 25
 NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 11550
 Contig ID 21672 1.R1040
 5'-most EST LIB3051-111-Q1-K1-E2

Seq. No. 11551
 Contig ID 21674 1.R1040
 5'-most EST uC-gmrominsoy069a01b1
 Method BLASTX
 NCBI GI g1717871
 BLAST score 577
 E value 2.0e-59
 Match length 259
 % identity 45
 NCBI Description UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15) >gi_1078006_pir_S53974 hypothetical protein YMR304w - yeast (Saccharomyces cerevisiae) >gi_798946_emb_CAA89137_ (Z49212) unknown [Saccharomyces cerevisiae]

Seq. No. 11552
 Contig ID 21675 1.R1040
 5'-most EST LIB3170-011-Q1-K1-B10
 Method BLASTX
 NCBI GI g2244993
 BLAST score 316
 E value 6.0e-29
 Match length 91
 % identity 66
 NCBI Description (Z97341) similarity to AMP-activated protein kinase beta [Arabidopsis thaliana]

Seq. No. 11553
 Contig ID 21677 1.R1040
 5'-most EST jex700905308.h1

